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Release 2.1D John F. Copyright (C) 1993, 1 Distribution	John F. Collins, Biocomputing Research Unit. 1993, 1994, 1995 University of Edinburgh, U.K. ibution rights by IntelliGenetics, Inc.
Psrch_nn n.a. · n.a.	database search, using Smith-Waterman algorithm
Ψ	2 16:57:20 1997; MasPar time 425.56 Seconds 1200.068 Million cell updates/sec
ular output not generated title: >US-08-915-	ated. 915-004-12 from mcA8915004 sea
e: 465 e: 1	TGAACAAGTTGCTGT
coring table: TABLE d	default
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earched: 362067	segs, 549138275 bases x 2
ost-processing: Minimum Listing	Match 0% first 45 summaries
atabase: embl-new	-new3 BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
1/:VIK atabase: genbank99 18:BCT1 25:BCT8	19:BCT2 20:BCT3 21:BCT4 22:BCT5 3 26:BCT9 27:BCT10 28:BCT11 29:GEN
31:GE 38:IN 45:IN	:HTG1 33:HTG2 34:HTG :INV5 40:INV6 41:INV 6:MAM1 47:MAM2 48:MA
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105:YKLLU genbank-new3 106:BCT 10 112:MAM 11	:VKLLV NCT NOT:GENI 108:GENZ 109:HTG1 110:HTG2 111:INV :MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRIZ
118:ROD natabase: u-embl50 122:par	0 119:SYN -99 :t1
Statistics: Mean 10	10.226; Variance 3.862; scale 2.648
Pred. No. is the number of score greater than or equal and is derived by analysis	number of results predicted by chance to have a in or equal to the score of the result being printed, analysis of the total score distribution.

SUMMARIES

Pred. No.	7.85e-05 7.85e-05	.13e-0 .94e-0	34e+0	34e+0	.34e+U	.34e+(.34e+0	.34e+	34e+(.84e+(.84e+(.84e+(84e+(5.84e	5.84e+(2.41e+(2.41e+	2.41e+(2.41e+01	2.41e-	2.41e+01	2.41e+	2.41e+	2.41e+	2.41e+01	2.41e+01 2.41e+01	2.41e+01	2.41e+01	2.41e+01 2.41e+01		-OCT-1996		r use to		
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Eur. J. Cell Biol. 57 (1), 66-74 (1992) 92347374
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1856 c 1799 g 1.
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Jacobs, H.T.T.T.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                   Gaps
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Zauner, W., Kratz, J., Staunton, J., Feick, P. and Wiche, G.
Identification of two distinct microtubule binding domains on
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their
6.0%; Score 28; DB 57; Length 215; 13.0%; Pred. No. 7.85e-05;
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Patent: US 5569830-A 5 29-OCT-1996;
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TITLE
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GMALNLEPDNVGVVVFGNDKLIKEGDVVKRSGAIVDVPVGESILGRVVDALGTPIDGK
Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry, University of Vienna, Waehringerstrasse 17, 1090 Vienna, AUSTRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase
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S.purpuratus nuclear gene for mitochondrial ATP synthase subunit
alpha precursor.
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Strongylocentrotus purpuratus
Bukaryotae; Mitochondrial eukaryotes; Metazoa; Echinodermata;
Bukaryotae; mitochondrial eukaryotes; Metazoa; Echinoida;
Strongylocentrotidae; Euechinoidea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
I (bases 1 to 2356)
Talamillo, A., Chisholm, A.A.K., Garesse, R. and Jacobs, H.T.
Expression of the nuclear gene encoding mitochondrial ATP synthasubunit alpha in early development of Drosophila and sea urchin
                                                                                                                                                               Direct Submission
Submitted (07-AUG-1992) G. Wiche, Institute of Biochemistry and
Molecular Biology, University of Vienna, Dr. Bohrgasse 9, 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="mitochondrial ATP synthase alpha subunit
precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Strongylocentrotus purpuratus"
/dev_stage="embryo (early blastula, 14 hours)"
/clone_lib="lambda ZAP, EH Davidson lab"
43..177
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mitochondrial ATP synthase alpha subunit; precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 92; Length 709
Pred. No. 6.13e-02;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1004 gcaaggaaatgcagtatttcatgcagcagtggactggaaccaacaa 1049
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ALEVAR NICHELER CLUSANON ELECTRATE ELUCA FELLINA ELUCA ALEVARIA EL CONTROLOGIONAL POR CENTRA ALEVARIA EL CONTROLOGIONAL EL CARANTIKGOLK FENDY VOORNINERVERMOSOGIONAL EL GASPINYRDPIGLIPLIYY VYSILGGGAHVDFRINSEQOTAMHKAAFLSSFENVYTLI ELGASPINYRDPIGLIPLIYY VYSILGGGAHVDFRINSEGOTAMHKAAFLSSFENVYTLI ELGASPINYRDPIGLIPLIYY NYNGNOVAELLILERAADIGYTDMHGNIBEI HQARKNEJTHYGHTPETTA FGGOLDAE NYNGNSPELHYCANINP ECARVLLFRGADHLAVNKGGGATAAHETHYSHIYGHNGYNBYDA NYNGNSPETTI PSEYGTMRSGMDSMRGGGMIAAGHETHINSHIYTPRGWRGFGFILL RSFRSSRTTITERVITUDYADMSRGGTIYHRPPTDTHDARGYDYYRAPSGFFILL BESRHASYRGOTITLKY TUTDYADMSRGGTIYHRPPTDTHDARGYDYYRAPNETRROSSHD SVSDMKRRGGGNAVAELRAGOSPYOMOYDGGELMGGYSSKYN SCSRHASYRGORGSRIS SAALLAYRGRYBSTROGASPYOMOYDGGELMGYSSKKYN BESRHASYRGRBSTRERFRYTSTRYRTSTROMATHAYSFD DEDEMPAPPPROGANSSTRONDSSTORED DEDEMPAPPRASYI SPDLORDSSSYRPRPTSTRYRTSTROMATHAYSFD OQQHPSLIRASSTSTRONDSSTORED PROGANNINGYROND STANDSTRONDS OQQHPSLIRASSATTOPPROGANSTRONDSSTORED PROGANNINGY AND SERVETSA
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GEIRCSEISFEHKKVDVWSVDDVIGWLSSLHLSEYTPAFRSQRINGRCLRQCDRSRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASVSNNNNNNNSTTDFQMDLKNALAKRSKVAHDVDEDEERESRFEGLSLRETVREN
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FDFDGRFWYKGGGNGTLNSAARFPLTLSDPNBRAPYTFKYLNYMADRHMHYGHVVPNV
NLFVYGKDKIMFRLMQNRLNPTMVG"
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/translation-"MNOEEDTVNLQIEVPELNVRKFLAVTQNDFIWDVRRKLLATLPQ
/translation-"MNOEEDTVNLQIEVPELNVRKFLAVTQUNFYWLMLDEK
ALPQAFNYGLFLPPPCDGRAGKFLLEDRIIRDVFANTONATORINGAN
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KAGQKPQTVPDVSLPGQTASFTGRSAFNPFTHMVSAVYTEDLVDAWGAGFAVNGVNNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKTETNADILLINRIDLDETAIDAAPFQLVIGSSLYKVHTLESLLGISHAYYTDCGKL
VGVVGLKELRDAMAITYRGAVAPVKPDRKLTSGTFLDMSHMNKDKLLNTPQTPPANG
LSINMESPKFGNSLTVPPMAL"
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/db_xref="P1D:g1066899"
/translation="DHVESNETFAEFCTRQAQNVVHFLVEDWFLSALLGIITAVLSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The start of this sequence (1..100) overlaps with the end of sequence CEBO491.
The end of this sequence (30012..30112) overlaps with the start of sequence CEC05D12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(4885..5105,5542..5761,5808..5895,
5947..6127,6408..6603))
/note="weak similarity with the E. coli outer membrane
protein FAED (Swiss Prot accession number P06970)"
                                                                                                                                                                                                                                                                                                                                                                                                      join (1...4) 413...532,582..713,1122..1255,1465..1555,
1773..1844,1889...2204,2251..2494,2539...2629,2683...2867,
2916..3168,3214..3361,3418..3643,3693...3881,4265..4480)
/note="similar to chloride channel protein"
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/clone="C33B4"
                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                               chromosome="II"
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2 (bases 1 to 30112)

2 (bases 1 to 30112)

3 Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Ranton, A., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Laister, N., Laisten, J., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, M., Parsons, J., Therry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Current sequence finishing criteria for the C. elegans genome current sequenced unambiguously consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIONS SECURITY THIS SEQUENCE IS NOT NECESSAILY THE ENTIRE INSERT OF CLONE C13B4. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone C13B4 is at 1 in this sequence. The true right end of clone C13B4 is at 9858 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The true left end of clone C05D12 is at 30012 in this sequence. The true right end of clone B0491 is at 4602 in this sequence. Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green, ms in preparation), and other
                                                      VAIDTIINQKRFNDEAEEKNKLYCIVVÄIGOKRSTVAOIVKRIHDSDÄLKYTIIVSÄT
ASDAAPLOYLAPYSGCAMGEFFRDNGKHALIIYDDLSKQAVAYRQMSLLLRRPPGREA
YPGDVFYLHSRLLERAAKMNPDFGGGSLTALPVIETOAGDVSAYIPTNYISITDGQIF
LETELFYKGIPPAINVGLSVSRYGSAAQVKAMKQVAGSMKLDLGEYREVAAFAQFGSD
                  GPLGTEHRARVGTKAPGIPRISVREPMQTGIKAVDSLVLICRGQRELIIGDRQTGKTA
                                                                                                                                                                                                                         LDASTONLLANGURLTELLKQGQYTPMAVEDQVAVLFAGVRGHLDKIDPAKVTKFEEQ
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditidae; Caenorhabditis.
I (bases 1 to 30112)
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/product-"mitochondrial ATP synthase alpha subunit
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                                                                                                                                                                                                                                                                                    FLAHIRSSHQALLDTIRTEGQLSPQTEATLKDVVLKFLDTFEG'
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Pred. No. 2.94e-01;
Transches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 others
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Caenorhabditis elegans cosmid C33B4.
248367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor"
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                                                                                                                                                                                                                                                                                                                                      178..1695
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REFERENCE AUTHORS

TITLE

COMMENT

ACCESSION KEYWORDS

SOURCE

SULT

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O'Rand, M.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="phosphoribulokinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGCGKSTEMRRATSIFGGVPREPPAGGNPDSNTLISDNTTVICLDDYHCLDRNGRKVKG
VTALAPERQNFDLMYNQVKALKEGKSVDKPIYNHVSGLIDAPEKIESPPILVIEGLHP
FYDKRVAELLDFKIYLDISDDIKFAWKIQRDMAERGHSLESIKSSIAARKPDFDAYID
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KLTCSFPGIKMFYGPDTWYGQEVSVLEMDGQFDKLEELIYVESHLSNTSAKFYGEITO
OMLKNSGFPGSNNGTGLFQTIVGLKVREVYERIVKKDVVPV"
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                                                                                                                                                                                                                                                                         phosphoribulokinase.
C.reinhardtii, cDNA to mRNA.
Chlamydomonas reinhardtii
Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Chlorophyta;
Chlorophyceae; Volvocales; Chlamydomonas.
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                                                                                                                                                                                                                          15-AUG-1990
                                                                                                     Gaps
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Euraryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eutaryotae; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 1256)
Richardson, R.T., Yamasaki, N. and O'Rand, M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 CAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACGCGTGTGCG 316
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Location/Qualifiers
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                                                                 Length 30112;
                                                                                                                                                                                                                             C.reinhardtii phosphoribulokinase mRNA, complete cds.
M36123
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                                                                         Pred. No. 2.94e-01;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 17; Indels
                                                                                                                 Db 14748 ctgtaaaaactattgtactttgcatgttactcattacttt 14788
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Chlamydomonas reinhardtii"
                                                                                                                                   MAM
                                                               Score 23; DB 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="phosphoribulokinase"
28.1155
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Pred. No. 1.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="phosphoribulokinase"
                   9126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 t
QLGVTRIAHRQIIESALRGLLQ
                  5799 g
                                                                                                                                                                                                                     mRNA
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                                                                                                                                                                                                                                                                                                                                                                   Roesler, K.R. and Ogren, W.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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O.cuniculus SP17 gene.
Z20655
                                                                                                                                                                                                                1245 bp
                                                           / Match
Local Similarity 78.0%;
les 32; Conservative
              5271 c
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Best Local Similarity 69.6%;
Matches | 39; Conservative
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                                                       Query Match
         BASE COUNT
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NILERREKTNFDPAEWGAKVDDRFYNNHAFORHESEKCEAEFKSGYTEEFTPVLTID
                                                                                                                                                  Submitted (21-7AN-1993) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090
                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-APR-1994) O'Rand M. G., University of North Carolina
at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel
Hill, North Carolina, USA, 27599-7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="3' untranslated region is identical for both 0.9 KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="alternate 5' untranslated region for 0.9 KB mRNA"
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Direct Submission
Submitted (26-NOV-1993) E.E. Powell, c/o John Todd, Level 6
Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="alternate 5'untranslated region for 1.1 KB mRNA" 607...1047
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-1995
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localization during the acrosome reaction
Dev. Biol. 165 (2), 688-701 (1994)
95046885
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryctolagus cuniculus"
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Pred. No. 1.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="New Zealand white"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="spermatogenic"
/clone_lib="Rabset"
/clone="SR-1&R-16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="testis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
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                                                                                                                                                                                                                     revised by [3] MAT
3 (bases 1 to 1256)
0'Rand, M.G.
                                                                                          (bases 1 to 1256)
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                                                                                                                                    Direct Submission
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111 TCAGCIGITGIGIGACAAATGICCICCIGGIACCIACCIAAAACAACACIGIACAGCAAA 170

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/Lodon_start=1
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/Lranslation="Linaga13831"
/Lranslation="Linaga13831"
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GPSQTPSILTSLGSTP11EQSTKGGISLIPIGLIYQYTSLGGILAMIGLYNDBARGHY
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QARVAALEAQCSQEARASSRISDSSHGSHGTHVNVTCIVNVCSSSDHSSQCSSQASATV
GDPDAKPSASPKDEQVPFSQEECPSQSPYETTETLQSHEKPLPLGVPDMGMKPSQAGW
                                                                                                                             Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A. Allelic variation of the type 2 tumor necrosis factor receptor gene Mamm. Genome 5 (11), 726-727 (1994)
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2 (bases 1 to 1388)
Powell,E.E., Wicker,L.S., Peterson,L.B. and Todd,J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is
linked to autoimmune diabetes in NOD mice
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Best Local Similarity 64.1%; Pred. No. 1.34e+00;
Matches 50; Conservative 0; Mismatches 28; Indels 0; Gaps
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/gene="murine tumour necrosis factor receptor 2"
/note="silent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(1262, "g")
/gene="murine tumour necrosis factor receptor 2"
/note="Thr to Cys"
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/note="silent"
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/note="Phe to Ile"
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/note="Ser to Thr"
replace(278,"t")
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                                                                                                                                                                                                                                                                                                                     /chromosome="4 (distal region)"
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                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                               Location/Qualifiers
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replace(975,"c")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(260, "c")
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                                                                                                 Unpublished
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//Tatailation="MATGHTVPAQVVLIPYKPEPGYEQISGEYYDRKAQMCCAKCP
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GDPDAKPSASPKDEQVPFSQEECPSGSFYETTETLQSHERPLFLGYPDMGMKRPSQAGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 1388)
Powell, E.E., Wickerf.L.S., Peterson, L.B. and Todd, J.A.
Allelic variation of the type 2 tumor necrosis factor receptor gene
Mamm. Genome 5 (11), 726-727 (1994)
                                                                                                                                                                                                                                                                                                                                                                       Powell, E.E.
Direct Submission
Submitted (26.NOV-1993) E.E. Powell, c/o John Todd, Level 6
Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK
Nuffield Dept 1388)
2 (bases 1 to 1388)
Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.
                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                        17-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid variation in the tumor Necrosis factor receptor 2 linked to autoimmune diabetes in NOD mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="murine tumour necrosis factor receptor 2"
/note="Ser to Thr"
/replace="c"
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M.musculus tumor necrosis factor receptor 2 mRNA.
X76401
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/strain="NOD"
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/replace="a"
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168 ctcggacaccgtgtgtgc 185
                              171 GIGGAAGACCGIGIGCGC 188
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VLCKACAPGTFSDTTSSTDVCRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYV
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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1 (bases 1 to 1505)

Lewis, M., Tartaqia, L.A., Lee, A.L., Bennett, G.L., Rice, G.C., Wong, G.H.W., Chen, E.Y. and Goeddel, D.V. Cloning and expression of cDNAs for two distinct murine necrosis factor receptors demonstrate one receptor is specific Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834 (1991)
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Mouse tumor necrosis factor receptor 2 mRNA, complete cds.
M60469
                                                    /gene="murine tumour necrosis factor receptor 2"
                                                                                                                               /gene="murine tumour necrosis factor receptor 2"
                                                                                                                                                                                                          /gene="murine tumour necrosis factor receptor 2"
/note="silent"
/replace="t"
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Pred. No. 1.34e+00;
0; Mismatches 28; Indels 0;
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Mus musculus
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/replace="t"
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/note="silent"
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Similarity 64.1%;
50; Conservative
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LGLWOLILTVQRKKRESCLGRDAKVPHVPDEKSQDAVGLEQGHLLTTAPSSSSSLES
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SDHSSQCSSQASATVGDPDARRSASKDEQVPFSQEECPSQSPCETTETLQSHEKPLP
LGVPDMGMKPSQAGWFDQIAVKVA"
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Adaxxef="TD:9202095"

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SBLSSQCSSQASAYVGDPDAKPSAPRDEQVPFSQEECFSQSPCETTETLQSHEKPLP
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOUUS MUSTNFR1 3796 bp mRNA ROD 01-AUG-1991
DEFINITION Murine tumor necrosis factor I receptor (TNFR-1) mRNA, complete
                                                                                                                                                                                                                                                                               193 tcagatgtgctgtgctaagtgtcctcctggccaatatgtgaaacatttctgcaacaagac 252
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Goodwin, R.G., Anderson, D.M., Jerzy, R., Davis, I., Brannan, C.I.,
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Pred. No. 1.34e+00;
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Pred. No. 1.34e+00;
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Mus musculus lymphoid cDNA to mRNA.
Mus musculus
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/tissue_type="lymphoid"
/map="Chromosome 4"
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microtubule-associated protein 1B.
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EVTKISQVEKTPRVESKEKVLVKKDREVKTESKEETP
EVTKISQVEKTPRVESKEKVLVKKDREVKEVTREKEVSKEEDSPVKAEVAEKO
ALESKPKVTKDVVKKEITKKLEEKKEEKPKKEVVKKEEKEPKKEIKLSKOSPVKAEVAEK
TPOSDTKKPSALKPVKKETPLKLOAKKEVKKEKKEVKKEEKEPKKEIKKISKDIKKS
AATTAAVVAAAGIAASGPVKELEARSCIMSPEDAGKLIKKOKKVKVTKKEGKTTAAATAVGT
AATTAAVVAAAGIAASGPVKELEARSCIMSPEDLIKDGEELKAEELDVAKDIKFOLE
LIEDEEKLKETQPGEAVVIQKETEVSKGSAESPDGGITTIGGEGECEQTPEELEPVEK
GOVDDIRKFEDDGAGFEESSETGDYEEKAETPEREEPEED
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Submitted (09-JAN-1990) Cowan N.J., Dept. of Biochemistry, New York
Submitted (09-JAN-1990) Cowan N.J., Dept. of Biochemistry, New York
University Medical Center, 550 First Avenue, New York, NY 10016
C (Dases 1 to 7620)
Noble,M., Lewis,S.A. and Cowan,N.J.
The microtubule binding domain of microtubule-associated protein
The microtubule and a repeated sequence motif unrelated to that of MAPP
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                               195 tcagatgtgctgtgctaagtgtcctcctggccaatatgtgaaacattctgcaacaagac 254
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       Gaps
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Mouse MAPIB mRNA for MAPIB microtubule-associated protein.
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54..7448
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/strain="Swiss Webster"
/dev_stage="5 day old"
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/clone_lib="lambda GEM"
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VNGFNALINGGSERKSCFWKLITRHLDRVDSILLTHIGDDNLPGINSMLQPK ABLEEE
OSGGSTTNSDMMKNLISPDLGVVFLWVPENLKNBPEPNIKMKSIEBAGFTLQYLNKLS
WLRPPLFRYGOFWIDPVLILEVENGVGKLEMYVLNPVKSSKEMQYFMQWTGTNKDKALE
PILPNGGEVDLPISYLTSVSSLIVWHPANPARKIIRVLFPGNSTQYNILEGLEKLKHL
DPLKQPLATQKDLIGQVPTPVVKQTKLKQRADSRESLKPAARPLPSKSVRKSKEETP
EVTKVNHVEKPPRVESKEKVMVKKDKFVKTETKPSVTEKEVPSKEEPPSFVKABYAEKQ
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biyteehlrraignielgirswdtnliecnldoelklfvsrhsarfspevpggkilhh
rsdyletyvlinpsdeavstevrlmitdaarhkllvlgocfentgelilosgsfsfo
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Human microtubule-associated protein 1B (MAP1B) gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSSSPVKKGDGKSKPLAASPKRCALKESSDKVSRVASPKKESVEKATKTTTPEVKA
TRGEEKOKETKNAANASASKSAKTATTGPGTTKTAKSSTVPPGLPVYLDLCYIPNHSN
SKNVDVEFFKRVRSSYYVVSGNDPAAEEPSRAVLDALLEGKAQMGSNMQVTLIPTHDS
                                                  DVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGVAEDTYSHMEGVASVSTAS
                                                                                                                 VATSSFPEPTTDDVSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECP
SSPVSDLTSTGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMSSQSALALDERKLGG
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Lien, L.L., Feener, C., Fischbach, N. and Kunkel, L.M.
Human MAP1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="transcription start at bp 166" /product="microtubule-associated protein 1B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVMREWYQETHEKQQDLNIMVLASSSTVVMQDESFPACKIEL"
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BEEYEPEKMEAEDYVWAVVDKAAEAGGAEEOYGFLTTPTKOLGAGSFGREPASSIHDE
TLPGGSESEATASDEBNREDOPEEFTATSGYTGSTIELSSEPTPMDEMGTPROVMSDE
TNNEETESPSOBEVNITKYESSLYSORYSKPADVTPLMGFSESKTDATDGKDYNASA
STISPPSSMEEDKFSALRANZCSEVKASTTLDIRGSISAVSEKVSBELSPS
PPSPLEKTPLGERSVNFSLTPNEIKYGARAFVAPVSFEVTORYVEERGASPEDRTLEY
VSPSOGYTGSAGHTPYYGSPTDEKSSHLPTEVIEKPPAVPVSFEFSDAKDENERASY
PMDEVPDSESPIEKVLSPLRSPLIGSESATESFLGADDKASGRAESPFEEKSGK
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EARODVDLCLVSSCEYKHPKTELSPSFINPNPLEWFASEEPTEESEKPLTQSGGAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGKQQGRQCDETPPTSVSESAPSQTDSDVPPETEECPSITADANIDSEDESETIFTD
KTVTYKHMDPPPAPVQDRSPSPRHPDVSMVDPEALAIEQNIGKALKKDLKEKTKTKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTKTKSSSPVKKSDGKSKPLAASPKPAGLKESSDKVSRVASPKKKESVEKAAKPTTTP
EVKAARGEEKDKETKNAANASASKSAKTATAGPGTTKTTKSSAVPPGLPVYLDLCYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHSNSKNVDVEFFKRVRSSYYVVSGNDPAAEEPSRAVLDALLEGKAQMGSNMQVTLIP
THDSEVMREWYQETHEKQQDLNIMVLASSSTVVMQDESFPACKIEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Betaherpesvirinae, Muromegalovirus.

1 (bases 1 to 13356)
Beuken, E., Slobbe, R., Bruggeman, C.A. and Vink, C.
Cloning and sequence analysis of the genes encoding DNA polymerase, glycoprotein B, ICP 18.5 and major DNA-binding protein of rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Beuken, E., Slobbe, R.,
Buugeman, C.A. and Vink, C.
Direct Submission
Submitted (05-MAR-1996) Cornells Vink, Medical Microbiology,
University of Limburg, PO Box 5800, Maastricht 6222 WH, The
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Pred. No. 1.34e+00;
0; Mismatches 12; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1514 gcaaggaaatgcagtattttatgcagcagtggactggtaccaacaa 1559
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96335691
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/organism="Rat cytomegalovirus"
/strain="Maastricht"
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Best Local Similarity 73.9%;
Matches 34; Conservative
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ACCESSION

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                                                                                                                                                                     GQLVPCLEEAVSVQIRSREGFKVPLYPATLFVPDGGRGDESGADASSSFGSSGDEEEE
VSPLLIDLIVDREFVGIVRIPMSCCDDGVLTRVTSFCPFVFLFYGTEDVLSSVEDHGD
                                                                             VRRLCEESRRRFGVRPFAPRRDREPTDVAALCRRLHLDPERTLGYVACGNGLKEMLYA
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RVRLRRGRRRPLGQQRRRAVRRPRRGGGGPGVRAGRTDDFSAVISSRGEADDAPLPO
PAQRRRGRRDLPQKRGRSK"
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TUTILIZATE I DE LE LOSTE EN TRECENDO DE LE LOSTE EN TRE L GVTRGDPPEAAAASSTTAPARGNNFALECGDPLLETTHDVNKEVNVRKRAYLKKVSEVG
NVVMACINSCHLUTKRLVNNNLVGTVCLEALSKVNNGFLSRQRATKEARALDDVGES
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CDS

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/note="similar to HCMV AD169 UL54, DNA polymerase, encoded by GenBank Accession Number X17403." /codon_start=1

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CDS

/product="DNA polymerase" /db_xref="PID:91255114"

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Caenorhabditis elegans

Bukaryotaes; mitochondrial eukaryotes; Metazoa; Nematoda;

Secarnentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoldea;

Rhabditidae; Caenorhabditis.

I (Bases It o 3759)

Nilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,

Bonfield, J., Button, J., Connell, M., Copsey, T., Cooper, J.,

Fulton, L., Caraton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jer, M.,

Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,

Latrellle, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,

Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopea, A.,

Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,

Vaughan, K., Waterston, R., Smaldon, N., Weinstock, L.,

Wilkinson-Stroat, J. and Wohldman, P.,

Nikinson-Stroat, J., and Wohldman, P.,

Nikinson-Stroat, J., and Wohldman, P.,

Nikinson-Stroat, J., A.,

Nikinson-Stroat, J.,

Nikinso
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VREAK IP I HAEKYFDQ I VKAVTINVLLPVFPKDMPRRERFFAYVLP I RTYLPEVFLRMS
KEDRECGAYLARESGLGMNSFIVYGEDTCGTG"
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                                                   ATGLIKTQCELSPRMFFEDREYVLDPVMVWPGLDIAADGEAVPPCDFVFHTFDQVVSL
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/translation="MDAEIFFNPYLHTKRSRRDWRAEPAADNKESFLQIVPRGVLYDG
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Pred. No. 1.34e+00;
0; Mismatches 18; Indels 0;
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Caenorhabditis elegans cosmid KOSB2.
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3 (bases 1 to 37599)
Waterston, R.
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Chissoe, S.
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Best Local Similarity 69.0%;
Matches 40; Conservative
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KEYWORDS

g S

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e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
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NEIGHBORING COSMID INFORMATION:
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The 5' cosmid is T07F12, 500bp overlap; 3' cosmid is ZK389. Actual start is at base position 1 of CELK05B2; actual end is at base position 37599 of CELK05B2.
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Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in preparation). Location/Qualifiers

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AKPYFHPKOTSTSSNYTSLPGRSAAGOQOLENGORSTSSLPTASAGGVTGTLGRNTR
PRPPGKYTSISIELKINLSRIFILKRSIYYIKAKYIDTISNYHI"
john (10249. 10398, 10355. 10585, 10834 . 10993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIKOOKNILRAILKPMIAANWPOOYOLELKKSHKIKASLAATKEAINKTKSDILKVEET

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COMPIGMENT (1901.11659, 11721...11996, 1355..1244,

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1344...13559,13754...14037,14094...14377,14894...14927))

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                                                                                                                                                                                                                                                                                    /codon_start=1
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FEATURES
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TITLE

COMMENT

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Search completed: Tue Dec 2 17:04:37 1997 Job time : 437 secs.

420 AAAATTAATTAGGATCATGCAAAGTCAGATAG 451

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1 ATGAACAAGTIGCTGTGCTG........TAAAAATAAGCTGCTTATAA 1089
TACTTGTTCAACGACACGAC......ATTTTTATTCGACGACAATATT
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23:EST212 24:EST227 25:EST223 26:EST224 27:EST225

28:EST226 29:EST227 30:EST223 36:EST239 32:EST230

33:EST231 34:EST237 35:EST233 36:ST51 37:EST230

46:ST31 47:ST52 41:ST56 42:ST57 43:ST58 44:ST59 45:ST510

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(MI)

    n.a. database search, using Smith-Waterman algorithm

                                                                                                                                                                                                           Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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æ	EFER	NCE	;	(bases	1; 1;	53		S))
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			Par	Sons	Į.	i i	n., Nacaba, L., Rohlfin	., Le, M., Lennou, S., (T., Soares, M., Tan,	יי יייייייייייייייייייייייייייייייייייי
			Treva	vaskis	[2]	Ę.	ston, R., Wi	liamson, A., Wohldman	n, P. and
	TITL	6-3	The	washu	Merc	ы	Project	•	
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Washington University School of Medicine

103:enEST29 104:enEST30 105:enEST31 106:enSTS 107:ueEST1108:ueEST2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

Result

Mean 11.077; Variance 1.866; scale 5.938

Statistics:

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/note="Organ: missing of the property of plasmid DNA from three normalized libraries (melanocyte 2NbHw, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 448.
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Contact: Wilson RK WashU-Merck EST Project Washington University
School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaškis E., Waterston R., Williamson A., Wohldmann P., Wilson
"The WashU-Merck EST Project";
Forest Park Parkway, Box 8501, St. Louis, MO 63108
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06-MAR-1997 (Rel. 51, Created)
06-MAR-1997 (Rel. 51, Last updated, Version 1)
2147908.rl Soares NhHMPu S1 Homo sapiens CDNA clone 666590 5'
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Verteprata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels (
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                                                                                                              Email: est@watson.wustl.edu
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1 Similarity 99.5%;
221; Conservative
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Fax: 314 286 1810
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/note="Organ: mixed (see below); Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZNDHM, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction
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Zr35a03.rl Soares NhHMPu Sl Homo sapiens cDNA clone 665356 5'.
AA195113
91784803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 448.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels (
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                                                                                                                Location/Qualifiers
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The WashU-Merck EST Project
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WashU-Merck EST Project
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Local Similarity 99.5%;
Wes 221; Conservative
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                                                                                                         J..530

/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Thom and filed polylinker; Site_1: Not I:
(Pharmacia) with a modified polylinker; Site_1: Not I:
(Site_2: Eco RI: Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NoHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewation.wustl.edu
This clone is avoilable royalty-free through LLNL; contact the
This clone is avoilable royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. High quality sequence stop: 257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA195113 530 bp mRNA EST 14-FEB-1997 2r35a03.r1 Soares NhHMPu S1 Homo sapiens CDNA clone 665356 5′. AA195113 91784803
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Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Pelman,M., Hulthan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74; DB 16; L
Pred. No. 6.00e-105;
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Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host-"DH10B"
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Best Local Similarity 100.0%;
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(Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHFU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIS sequence; primer; sequence tagged site. human Plasmid clones, generated from a lymphoblastoid cell line throm a human male. Localized to human chromosome 12 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Camden, NJ 08103.
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
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                                                                                                                                                                                                                                                                                                               /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH10B" <1..>530
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62 degrees C for 23 seconds
72 degrees C for 30 seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Pax: 4157259689
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0
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Pred. No. 6.00e-105;
0; Mismatches 0; Indels
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Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                       /clone_lib="Soares NhHMPu S1"
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human STS SHGC-13782 clone pG-6721.
G10922
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Primer B: TGGTGGGGAGTATCAGGTTC
STS size: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae; Homo.
1 (bases 1 to 400)
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Polymerization:
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Best Local Similarity 100.0%;
Matches 74; Conservative
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Terrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhin; Hominidae; Homo.
1 (bases 1 to 245)
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                                                                                                                                                                                                                                                                                                                                                           Whitehead Institute/MIT Center for Genome Research; Physically Mapped SISs
                                                                                                                         23-0CT-1995
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/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
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56..155
/map="791_B-4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whitehead Institute/ALT Center for Genome Research Whitehead Institute for Biomedical Research Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900

Eax: 617 252 1902

Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 245;
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Pred. No. 1.84e-03;
0; Mismatches 14; Indels
                                                                                                                       STS
                                                                                                                                                                                       SIS sequence; primer; sequence tagged site. human SISs derived from random genomic DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer A: TGTTIGTAGTTGTTTGTTATTTGGA Primer B: AAAGGAGTCAAAATGGGTTTTT STS size: 100 PCR Profile:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
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Primer: each 5 pM
dNTPs: each 4 nM
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MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
                                                                                                             G11923 245 bp
human STS MR4116.
G11923
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Best Local Similarity 70.8%;
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Physiol. 106:1241-1255(1994).

AGIS: T42477; AGIS July 1995.

Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, Mi Tel: 517.353-0854 Fax: 517-353-9168

Email: 22313tcn@lbm.cl.msu.edu. NCBI gi: 933235

Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 400;
                                                                                                                                                                                                                                                                                                                                                                                            6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Match
2.0%; Score 22; DB 77; Length 472;
Local Similarity 68.6%; Pred. No. 9.42e-05;
nes | 35; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ored. No. 9.42e-05;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/clone="113K157"
/strain="var columbia"
/note="thale cress"
Sequence 472 BP; 126 A; 97 C; 100 G; 137 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FFB-1995 (Rel. 42, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 15)
5740 Arabidopsis thaliana cDNA clone 113K15T7.
    each 200 uM
0.05 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 39;
Pred. No. 9.42e-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 aacctcaagaaagcaccccacacagggtaaaat 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               626 AACCIGAAGAAIGCCICCICACACAGGGIAACAI 593
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                 2.5 mM
50 mM
20 mM
                                                                                                                                                                                                                                                                                        /map="12"
230..250
/map="12"
complement(308..327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; RNA; EST; 472 BP.
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                           8
.3
                                                                                                                                                                                                                                                                                                                                                                                     63 g
dNTPs:
Tag Polymerase: C
Total Vol:
                                                                                                                                                                                           Chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.0%;
Best Local Similarity 82.4%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     91 c
                                                                                                                                                                                                                                                                                                                                                                     /map="12"
                                                                                                                                     Tris-HCl:
                                                                                                                                                                                                                                  1..400
                                                                                               MgC12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-472 |
MEDLINE; 95148729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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T42477;
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g cb

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LOCUS T03759 392 bp mRNA EST 14-FEB-1997
DEFINITION IB862 Infant brain, Bento Soares Homo sapiens cDNA clone IB862
3 end.
ACCESSION T03759
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wistl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llhi.gov) for further information. MGI:217450 Seq primer: mob.REGA+ET.
 Gaps
                                                                                                                                                                                                                                                                                                                                   Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Moris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                 04-MaY-1996 (Rel. 47, Created)
05-WAR-1997 (Rel. 51, Last updated, Version 2)
mb83g02.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 336050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 1.9%; Score 21; DB 90; Length 377; Local Similarity 88.9%; Pred. No. 1.84e-03; nes 24; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minoru KO (Wayne State University)."
/clone="336050"
/clone_lb="Soans mouse p3NMF19.5"
/dev_stage="19.5" dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA <1..>377 Sequence 377 BP; 109 A; 85 C; 94 G; 89 T; 0 other;
    ..
ω
                                123 acacageteacatgtacagacaataaaactgeteaag 159
                                                     729 ACACAGCTCACAAGAACAGACTTTCCAGCTGCTGAAG 765
      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 aaaatggaagccaagacaccttgaagg 61
                                                                                                                          standard; RNA; EST; 377 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.; "The Washu-HHMI Mouse EST Project";
                                                                                                                                                                                                                                                    Mus musculus (house mouse)
        29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
                                                                                                                LT 9
MM05110
W18051;
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/map="923_H_8: 959_F_5: 441.7 cR from top of Chr17 linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29..253
/map="923_H_8; 959_F_5; 441.7 cR from top of Chr17 linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="923_H_8; 959_F_5; 441.7 cR from top of Chr17 linkage
                                                                                                                                                                                                                         Eukaryotee; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata;
Tetrapoda; Amniota; Mammalla; Theria; Eutherla; Archonta; Primates;
                                                                                                                                                                                                                                                                                                                       Whitehead Institute/MIT Center for Genome Research; Physically
                                                                                                        19-0CT-1995
                                                                                                                                                                    STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prepared with primer pairs derived from 238433 -- dbEST. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 38; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
                                                                                                                                                                                                                                                                                                                                                                                               Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA
                Score 21; DB 38; 1 Pred. No. 1.84e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACAGTIGIGAAGCCGIGC
225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 g
                                                                                                                                                                                                                                                                              Catarrhini; Hominidae; Homo.
1 (bases 1 to 253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Template: 10 ng
Primer: each 5 pM
dNTPS: each 4 nM
                                                                                                                                                                                                                                                                                                                                                                                            Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.9%;
Best Local Similarity 78.4%;
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KCl: 50 mM
Tris-HCL: 10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total Vol: 20 ul
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                                                                                                                  253 bp
                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rel: 617 252 1900
Fax: 617 252 1902
                                                                                                                             human STS WI-6406.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer B: CAC
STS size: 225
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 a
                                                                                                                                                                                                                                                                                                                                            Mapped ESIS
                                                                                                                                                                                                             collection.
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                                                                                                                                    DEFINITION
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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Not1: The infant brain library, constructed by Bento Soares, Columbia University, was oligo-(dT) primed and directionally choned into an M13-derived plasmid using total brain maRNA from a 72-day old human female afflicted ...th critical miscuilar attochy.
                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 392)
Rhan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M. Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M13-derived; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zq16e09.sl Stratagene fetal retina 937202 Homo sapiens cDNA clone PROTEIN 1B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homindae; Homo. 1 (bases 1 to 431)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultnan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Waterston,R., Williamson,A., Wohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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WashU-Merck EST Project
WashIngton University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                    Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Eax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Infant brain, Bento Soares"
/lab_host="E. coli DH5-alpha"
complement(<1..>392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.9%; Score 21; DB 53; 1
Best Local Similarity 78.4%; Pred. No. 1.84e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 açacagetcacatgtacagacaataaaaetgetcaag 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729 AÇACAĞCICACAAĞAAĞAĞAĞAĞTITCCAĞCIĞCIĞAAĞ 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with spinal muscular atrophy./clone="IB862"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                           Nature Genet. 2, 180-185 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="D0S8967E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 bp
                                                                                                                                                                                                                                                                                   Contact: Sikela JM
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                                                                Homo sapiens
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AUTHORS
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Jacses 1 to 443)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anony Coronal unidirectionally, Primer: Oligo dr. Pooled retinal tissue. Average insert size: 1.0 kb; Uni-2AP XR Vector: -5' adaptor sequence: 5' GAATTGGGCAGGAG 3' -3' Alabone-"62986"  
'Clone-"62986"  
'Clone-"629886"  
'Clone-"62986"  
'Clone-"62986"  
'Clone-"62986"  
'Clone
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand possible reversed clone: polyT not found Seq primer: -41ml3 fwd. ET from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK-; Site_1: EcoR1; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Pool
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Vertebrata; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION mw82b02.rl Soares mouse NML Mus musculus cDNA clone 677163 5.
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WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
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Similarity 71.7%; Pred. No. 1.84e-03;
33; Conservative 0; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<1..>431)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 c
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Fax: 314 286 1810
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Best Local Similarity
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RESULT
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Racaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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   constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                   AA213094 443 bp mRNA EST 31-JAN-1997
mw82b02.r1 Soares mouse NML Mus musculus cDNA clone 677163 5'
AA213094
                                                                                                                                                                                                                                                                                                 31-JAN-1997
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.84e-03;
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Location/Qualifiers
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/clone_lib="Soares mouse NML"
/lab_host="DH10B"
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                                             /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project Unpublished (1996)
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                               /clone="677163"
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Matches 24; Conservative
                                                                                                                                                    Query Match 1.9%;
Best Local Similarity 88.9%;
Matches 24; Conservative
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                                                                                                          BASE COUNT
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                                                                                            mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATURES
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                                                                                                                           ORIGIN
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                             03.FEB-1997 (Rel. 50, Created)
20.FEB-1997 (Rel. 51, Last updated, Version 2)
mw82b02.rl Soares mouse NML Mus musculus cDNA clone 677163 5'.
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Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
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1.9%; Score 21; DB 98; Length 443
Best Local Similarity 88.9%; Pred. No. 1.84e-03;
Matches 24; Conservative 0; Mismatches 3; Indels
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Sequence 443 BP; 123 A; 105 C; 118 G; 97 T; 0 other;
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12-MAR-1997 (Rel. 51, Last updated, Version 9)
21953 Arabidopsis thaliana cDNA clone G8G4T7.
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MMAA13451 standard; RNA; EST; 443 BP.
AA213094;
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/lab_host="DH10B"
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223 aaaatggaagccaagacaccttgaagg 249
                                                 887 AAAATGGCGACCAAGACACCTTGAAGG 913
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                                           A MEDLINE: 95148729.
RA MEDLINE: Wedgettin F.J., Green P., Keegstra K., Kende H.,
RA McIntosh L., Ohlrogge J., Raikhel N., Somerville S., Thomashow M.,
RA Retzel E., Somerville C.,
RT Grees galore: a summary of methods for accessing results from
RT large-scale partial sequencing of anonymous Arabidopsis cDNA
RT large-scale partial sequencing of anonymous Arabidopsis cDNA
RL Dant Physiol. 106:1241-1255(1994).
CC Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan
CC Contact: Thomas Newman MSU-DOE PRL, Michigan State University, Plant
CC State University MSU-DOE-PRL, Michigan State University, Plant
CC Email: 22313tcn@thom.cl.msu.edu. NCBI gi: 1269126
F. Key
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Best Local Similarity 80.0%; Pred. No. 1.84e-03;
Matches 28; Conservative 0; Mismatches 7; Indels
 Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                   /Organism="Arabidopsis thaliana"
/Clone="G8G4T7"
/Strain="var columbia"
/note="thale cress"
/note="thale cress"
/1.>496
Sequence 496 BP; 132 A; 87 C; 124 G; 137 T; 16 other;
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Search completed: Tue Dec 2 16:56:58 1997 Job time : | 325 secs.

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TACTTGTTCAACGACACGAC......ATTTTTATTGACGACAATATT
                                                                        | 1.EST1 2.EST2 3.EST3 4.EST4 5.EST5 6.EST6 7.EST7 8.EST8 |
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| 1.EST15 10.EST10 11.EST17 12.EST12 13.EST13 14.EST14 |
| 1.EST15 10.EST10 11.EST17 12.EST12 13.EST13 14.EST14 |
| 2.EST21 22.EST22 23.EST23 24.EST24 25.EST25 26.EST26 27.EST27 28.EST38 33.EST33 38.EST33 38.EST38 38.EST38 38.EST38 38.EST38 39.EST39 40.EST40 41.EST41 42.EST42 43.EST43 44.EST44 45.EST45 46.EST46 47.EST47 48.EST42 43.EST43 44.EST44 45.EST55 56.EST56 57.EST57 58.EST57 58.EST57 58.EST57 58.EST57 56.EST67 66.EST66 61.EST61 62.EST66 63.EST68 64.EST64 65.EST66 66.EST66 61.EST67 61.EST70 77.EST77 78.EST77 74.EST77 74.EST77 74.EST77 78.EST77 78.EST77 78.EST78 74.EST74 77.EST77 78.EST79 80.EST86 87.EST99 84.EST99 94.EST99 94.EST99 94.EST99 94.EST99 94.EST99 94.EST99 94.EST99 94.EST99 94.EST99 94.EST919 14.EST110 105.EST10 11.EST110 11.EST111 112.EST112 113.EST113 114.EST110 115.EST110 116.EST110 116.EST110 117.EST117 118.EST113 114.EST119 115.EST112 114.EST114 115.EST112 114.EST114 115.EST113 114.EST114 115.EST113 114.EST114 115.EST115 114.EST114 114.EST115 114.EST115 114.EST115 114.EST115 114.EST115 114.EST115 114.EST115 115.EST115 114.EST115 114.EST115 114.EST115 114.EST115 114.EST115 114.EST115 114.E
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(MI)
                                                                                                                                                                                                                                                                                                          n.a. - n.a. database search, using Smith-Waterman algorithm
                                                                                                                                             Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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(1-1089) from US08915004.seq
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Statistics: Mean 11.043; Variance 1.850; scale 5.968

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ACCESSION	AA037313								
NID	g1512420								
KEYWORDS	EST.								

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BCO RI datapers (Pharmacia), digested with Not I and Conced into the Not I and Eco RI sites of a modified pr773 vector (Pharmacia). Library went through one round of normalization to a cot = 5. Library constructed by Bento Scares and M.Fatima Bonaldo. Library constructed by Bento Aclone—1359973 Seness senescent fibroblasts Norse. // Alsue_type="senescent fibroblast" // Library constructed by Aclone—11b-"Soares senescent fibroblasts Norse. // Alsue_type="senescent fibroblast" // Albab.bost="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1203 Std Brror: 0.00 Seq primer: -28413 rev2 from Amersham High quality sequence stop: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 602) Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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human clone=253126 primer=M13RP1 library=Morton Fetal Cochlea vector=pBluescript SR - host=SOLR cells (kanamycin resistant) Rsitel=EcoRI Rsite2=XNoI The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends. adaptor linker: GAATTCGGCACGAG.
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1 (bases 1 to 346)
11 (bases 1 to 346)
12 (bases 1 to 346)
13 (bases 1 to 346)
14 (bases 1 to 346)
15 (bases 1 to 346)
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gg78954
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
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Washb-Merck EST Project
Washbgton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Email: escewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 258.
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Toward cataloguing all rice genes: large-scale sequencing of randomly chosen rice cDNAs from a callus cDNA library lant.
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1 (bases 1 to 330)

Sasaki, T. and Minobe, Y.

Rice cDNA from callus
Unpublished (1993)
                                                                                              Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Oryza sativa (strain Nipponbare, ) callus cDNA to mRNA
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/sex="female"
/dev_stage="HeLa S3 cell line"
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Pred. No. 1.45e-04;
0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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Matches 37; Conservative
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Phone:0298-38-7441
Fax: 0298-38-7468
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Fax: 314 286 1810
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygii, Choanata, Tetrapoda, Amniota, Mammalla, Theria,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 300)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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old male. 1st strand cDNA was primed with a Not I primer [5,
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Matches 28; Conservative
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1996
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
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                                                                                                                                                                                                                                                                                                                                                                             938 GAGTGCTTTAGTGCGTGCATTAGGCCCTTCAAGGTGTCTTGGTCGCCATTTTT 885
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0
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Homo sapiens fetus brain cDNA to mRNA, clone:093D09.
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                                                                                                                                                                                                                                           Length 330;
                                                                                                                                                                                                                                                                                                     0; Mismatches 16; Indels
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                                                                                                                                                                                                                                       Score 22; DB 13;
Pred. No. 1.45e-04;
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Human fetal brain cDNA 5'-end GEN-093D09
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                            /organism="Oryza sativa"
/strain="Nipponbare"
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                                                                                                 /tissue_type="callus"
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83 c 75 g
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                                                                                                                                                                                                                                       2.0%;
llarity 70.4%;
Conservative
                                                                                                                              47 C
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Best Local Similarity
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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT2; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. 10.5dpc
                                                                                                                                                                 Washugton University School of MedicineP Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information.
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/dev_stage="10.5dpc embryos"
/lab_host="DH10B"
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[ bases 1 to 410)

Hilliar,L. Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 180; Length 385;
Pred. No. 1.45e-04;
0; Mismatches 3; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              embryos. pCMV-SPORT2 vector." /clone="553259"
                                                                                                                                                                                                                                                                                                                                                       Trace considered overall poor quality Seq primer: -28M13 rev1 from Amersham High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Mus musculus"
                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J
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WashU-Merck EST Project
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Local Similarity 89.3%;
Les 25; Conservative
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                                                                                                            Unpublished (1996)
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Eucaryotae: Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (pases 1 to 465) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Milliamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                            Email: estewatson.wustl.edu
High quailty sequence stops: 232
Source: IMAGE Consortium, LLNL
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                         15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                   Length 453;
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9933235
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177351
g694554
Score 22; DB 111; Le
Pred. No. 1.45e-04;
                                                                                          273 ggacacgtttcctgggtggccgctttgatgatgttgtcca 312
                                                                                                                            74 GGAAACGITICCIGGGIGGICCACITAATGGAGAIGICCA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
Other_ESTs: yd72e10.s1
Contact: Wilson RK
WashU-Merck EST Project
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Similarity 82.4%;
28; Conservative
             2.0%;
Best Local Similarity 77.5%;
Matches 31; Conservative
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcoptersygli; Choanata; Terrapoda; Amniota; Mammalla; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Hearston, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washbrymerck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand.
   Fax: 314 286 1810
Email: est@watson.wustl.edu
High qailty sequence stops: 212
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N21157 453 bp mRNA EST 19-DEC-1995 yx47d01.sl Homo sapiens cDNA clone 264865 3' similar to SP:ICPB_MOUSE P80314 T-COMPLEX PROTEIN 1, BETA SUBUNIT ;
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Pred. No. 1.45e-04;
0; Mismatches 7; Indels
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/clone="264865"
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57 c
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Matches 29; Conservative
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Arabidopsis thallane Europhyta: Magnoliophyta: Magnoliopsida; Capparales; Buzyotae; Enbryophyta: Magnoliophyta: Magnoliophyta: Magnoliophyta: Magnoliophyta: Magnoliophyta: Eucaryotae; Enbryophyta: Magnoliophyta: Magnoliophyta: Capparales; I (bases 1 to 412)

Newman,T., de Bruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etholated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark. rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUL-1995
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/clone="113K157"
/strain="var columbia"
1 97 c 100 g 137 t
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PROJECT = 'RGP'
Submitted (14-Feb-1995) to DDBJ by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu.
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Best Local Similarity 68.6%;
Matches 35; Conservative
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Phone: 0298-38-7441
Fax : 0298-38-7468.
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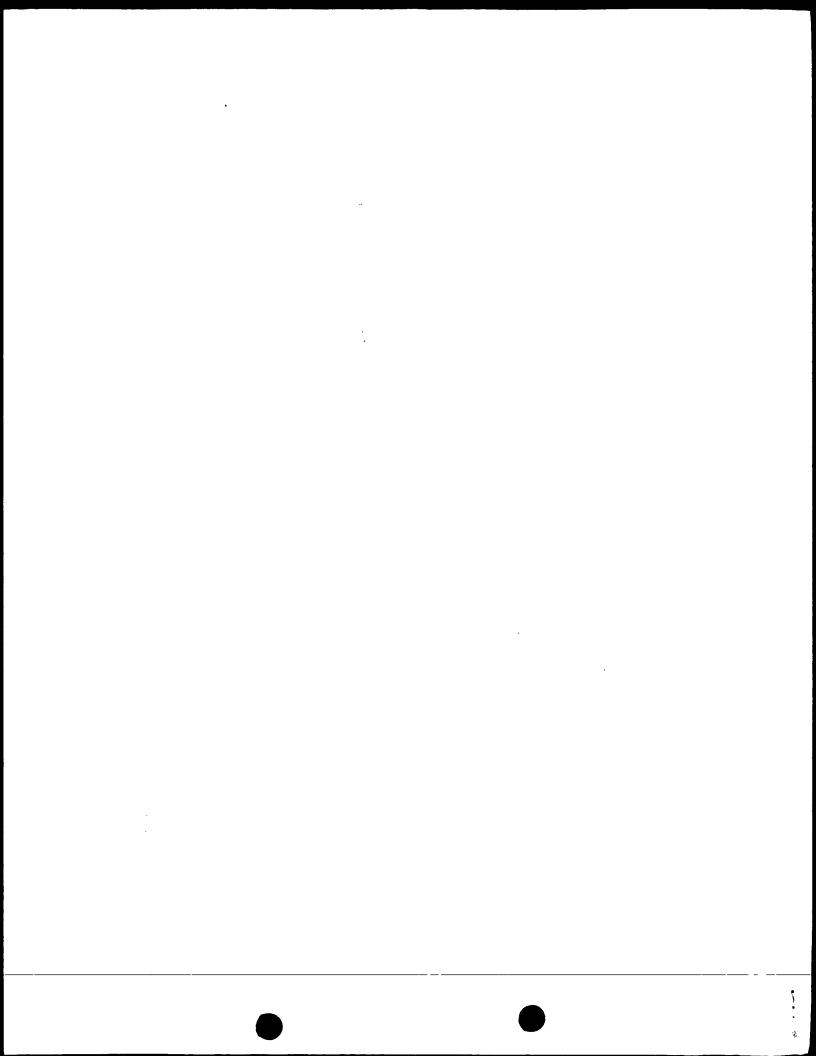
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/organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Corgan: eye; Vector: lambda gtl0; Site_l: EcoRI;
//orte="Corgan: eye; Vector: lambda gtl0; Site_l: EcoRI;
//orte="Corgan: eye; Vector: lambda as a
Sublibrary derived from a human retina cDNA library
Inserts from retina cDNA library DNA were isolated,
randomly primed, PCR amplified, size-selected, and cloned
into lambda gtl0. Individual plaques were arrayed and
used as templates for PCR amplification, and these PCR
products were used for sequencing."
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55c10 Human retina cDNA randomly primed sublibrary Homo sapiens
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
Macke, J., Smallwood, P. and Nathans, J.
Adult Huma Retina cDNA
Unpublished (1996)
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Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
JS North Wolfe Street, Baltimore, MD 21205
Tel: 410 055 4678
                                                                                                                                                                                                     388 cgggtgcantnacggcaaccaggtgctcaaggagctngaggaggccaagaaggngt 443
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Pred. No. 1.45e-04;
0; Mismatches 12; Indels
                                                                                                                        Length 493;
                                                   5 others
                                                                                                                                                                0; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCACAA 305
/strain="Nipponbare"
/dev_stage="Green shoot (8 days old)"
147 c 150 g 93 t 5 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORMARD: CITITGAGGAAGITCAGCCTGGITAAGT
BACKWARD: GAGGTGGAATATGAGTATTCTTCCAGGGTAA
Seq primer: GGGTAAAAAAGAAAT.
Location/Qualifiers
                                                                                                                     Score 22; DB 55;
Pred. No. 1.45e-04;
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/dev_stage="adult"
/lab_host="E. coli strain K802"
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                                                                                                                Query Match 2.0%;
Best Local Similarity 66.1%;
Matches 37; Conservative
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Best Local Similarity 73.9%;
Matches 34; Conservative
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δ
                                                                                                                                                                                                                                                             Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
                                                                                                                                                                                                                                                                                                                                                                                                                          ** (bases 1 to 253)
Auffray, C., Botar, G., Bots, F., Bouchier, C., da Silva, C.,
Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,
Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
Sebastiani-Rabaktchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone library from B.Soares, Psychiatry Dept. Columbia University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human clone=110433 library=Soares fetal liver spleen lNFLS vector=p17T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=-21m13 Rsitel=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-1995
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                                                                                                                      Homo sapiens
Msaryotes, mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 253)
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stretch_removed: 31 T removed at sequence 5'end
Normalization_method: Bento Soares, P.N.A.S in press;
Genexpress_library_idt: C;
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Pred. No. 2.90e-03;
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/isolate="muscular atrophy patient"
/dev_stage="3 months old"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
       sapiens partial cDNA sequence; clone c-Obe06
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Primer: (-21)M13_universal;
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                                                                         partial cDNA sequence; transcribed sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No significant homology found with : genbank release 81 swissprot release 28. Location/Qualifiers
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Eucaryotas; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 265)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Rucabb, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATAATAAAGATCTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pr773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Faxil: est@watson.wustl.edu
High quality sequence stops: 241
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 265;
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Pred. No. 2.90e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-Merck EST Project
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61 c 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
WashU-Merck EST Project
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Best Local Similarity 66.7%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
                                                                                                                                                                           Homo sapiens
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US-08-915-004-10.rng

*** (WL)
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Tue Dec 2 16:36:04 1997; MasPar time 121.52 Seconds 935.265 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-10 (1-1089) from US08915004.seq 1089 Description: Perfect Score: N.A. Sequence: tle:

1 ATGAACAAGTIGCTGTGCTG.......TAAAAATAAGCTGCTTATAA 1089
TACTTGTTCAACGACACGAC......AITTTTATTCGACGAATATT Comp:

TABLE default Gap 6 Scoring table:

142080 seqs, 52183452 bases x 2 Searched:

Dbase 0; Query 0

STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq28
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28

Mean 9.038; Variance 4.941; scale 1.829 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4		æ					
NO.	Score	Watch	watch Length	DB	ΙD	Description	Pred. No
Н	871	80.0	1173	28	T35475	Human tumour necrosis	0.00e+00
7	869	79.8	996	27	T33179	Mutated OCIF, OCIF-CS	
m	869	79.8	1056	27	T33173		_
4	869	79.8	1182	27	T33178	OCIF,	_
ഗ	869	79.8	1200	27	T33172	Mutated OCIF, OCIF-CL	Ĭ
9	869	79.8	1206	27	T33164	OCIF,	Ĭ
7	869	79.8	1206	28	T36685	Osteoclastogenesis in	_
ω	867	79.6	1206	27	T33165	Mutated OCIF, OCIF-C2	_
σ	865	79.4	1206	78	T33162	Mutated OCIF, OCIF-C2	_
10	865	79.4	1206	27	T33163	Mutated OCIF, OCIF-C2	_
11	865	79.4	1206	5 8	T33161	Mutated OCIF, OCIF-C1	_
12	816	74.9	984	27	T33171	Mutated OCIF, OCIF-DD	0.00e+00
13	814	74.7	819	27	T33174	Mutated OCIF, OCIF-CD	0.00e+00
14	682	62.6	1083	27	T33166	Mutated OCIF, OCIF-DC	0.00e+00
15	598	54.9	981	27	T33170	Mutated OCIF, OCIF-DD	0.00e+00

				0.00e+00	.00e+0	•	2.81e-2	2.67e-2	1.10e-2	1.10e-16	2.55e-3	1.12e-2	.20e-1	.22e-1	4.06e-10	7.06e-09	.90e-0	.90e-0	2.90e-08	.17e-0	4.71e-07	.86e-0	1.86e-06	.86e-0	.26e-0	.26e-0	.26e-0	2.79e-05	.06e-0
OCIF, OCIF-C	Mutated OCIF, OCIF-CB	OCIF, OCIF-		ted OCIF, OCIF-	OCIF-	saus	Osteoclastogenesis in	Fragment of human OCI	Mutated OCIF, OCIF-CC	Mutated OCIF, OCIF-CP	Human Natriuretic Pep	Human Natriuretic Pep	Oligonucleotide probe	Base substituted E.co	Oligonucleotide probe		Generic DNA sequence	٠,	Generic DNA sequence	Generic DNA sequence	ic DNA :	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	eneric DNA s	Generic DNA sequence	ic DNA s	eneric DNA sequen	c DNA s
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ALIGNMENTS

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for treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation claim 1; Fig 1; Spp; English.

The receptor binds to INF, and in particular, TNF-beta.

The receptor may be used for screening for antagonists and agonists of the receptor and for ligands for the receptor. Such agonists be used to inhibit the growth of tumours, to stimulate cellular
                                                05-MAY-1997 (first entry)

Human tumour necrosis factor receptor.

Tumour necrosis facor; TNF; receptor; TNF-beta; ligand; tumour; differentiation; immune response; autoimmune disease; inflammation; septic shock; graft-versus-host; apoptosis; ss.

Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft-versus-host reactions, and to prevent apoptosis.

Sequence 1173 BP; 374 A; 277 C; 265 G; 257 T;
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                     15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
(HUMA-) HUMAN GENOME SCI INC.
Fleischmann RD, Greene JM;
WPI; 96-433821/43.
.r 1
T35475 standard; cDNA; 1173 BP
                                                                                                                                                                                                         1..1173
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WO9628546-Al.
                                                                                                                                                                   sig_peptide
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CDS
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Query Match

80.0%; Score 871; DB 28; Length 1173;

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Mutated OCIF, OCIF-CSph, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
Synthetic.
Location/Qualifiers
                                                                                                 cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagaatagagttctgcttgaaa 360
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                                                                                                                                                                                                                          ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300
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                                           atgaacaagttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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                      0; Gaps
                                                                1 ATGAACAAGTIGCIGTGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC
                                                                                      caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg
                                                                                                                                                                                gtgtgcgcccttgccctgaccactactacagacagacagcacaccagtgacgagtgt
                                                                                                                                                                                                                                       241 CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC
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          Pred. No. 0.00e+
0; Mismatches
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         Similarity 100.0%;
871; Conservative
           Best Local
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PARTICLE, NOTAGE, 187949.

DNA encounted gosteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 81; Page 169; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CSph in which amino acids 298-380 of the mature protein have been deleted and replaced by Ser-Leu-Asp. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 KD under reducing conditions and 120 KD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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a M, Yano
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20-FEB-1995, J00374.
20-FEB-1995, JP-054977.
21-UUL-1995, JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochi:
1..63
                                                                                                                        OCIF-CSph
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CC in which amino acids 311-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 6 Nb under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and
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                                                                                                                                                                               aacaaagaccaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteoporosis; ss.
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               541 CACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGGAATAGATGTTACC
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Sequence 1056 BP; 332 A; 252 C; 247 G; 225 T;
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20-FEB-1995; JP-054507.
20-FEB-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GGLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                     841 gtgcagcggcacattggacatgctaacctca 871
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22-APR-1997 (first entry)
Mutated OCIF, OCIF-CBst, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
121 tgtgacaaatgteeteetggtacetacetaaaacaacactgtacagcaaagtggaagaee
                   Cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa
                                                                                                                                                                                                                                                                            cataggagctgcctcctggatttggagtggtgcaagctggaaccccagagcgaataca
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                                                                      gtgtgcgcccttgccctgaccactactacagagacagctggcacaccagtgacgagtgt
                                                                                                                                          ctatactgcagcccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
                                                                                                                                                                                                                                 361 CATAGGAGCTGCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACA
                                                                                                                                                                                                                                                                                                                                               421 gtttgcaaaagatgtccagatgggttcttctcaaatgagacgtcatctaaagcaccctgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 cacgacaacatatgttccggaaacagtgaatcaactcaaaaaatgtggaatagttacc
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                                                                                                                                                                                                                                                                                                                                                                                                                     481 agaaaacacacaaattgcagtgtctttggtctcctgctaactcagaaaggaaatgcaaca
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T33178 standard; DNA; 1182 BP
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29-Aug-1996.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
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                                                                                                                   for bone resorption control, esp. treatment of osteoporosis Claim 78; Page 148; 183pp; Japanese.
                                   Morinaga T
                            Gotol M. Higashio K. Kobayashi F. Mochizuki S. Morinaga
Nakagawa N. Shima N. Tsuda E. Ueda M. Yano K. Yasuda H.
Wapi je 402320/40.
P-PSDB: R99948.
DNA encoding osteoclastogenesis inhibitory factor protein
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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Best Local S
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone rescription control, esp. treatment of osteoporosis claim 60; Page 143-144; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CL in which amino acids 379-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.

Sequence 1200 BP; 387 A; 283 C; 268 G; 262 T;
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Mutated OCIF, OCIF-CL, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
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29-AUG-1996, J00374.

R 20-FEB-1995, JP-054977.

PR 21-JUL-1995, JP-207508.

PA (SNOW ) SNOW BRAND MILK PROD CO LTD.

GOLO M, H4gashio K, Kobaysshi F, Mochizuki S, Morando M, Kana K, Tsuda E, Ueda M, Yano K, Yan
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T33172 standard; DNA; 1200 BP.
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22-APR-1997
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Mutated OCIF., OCIF-C22S, coding sequence.
OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
 ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
                                                                                                                                                                  useful
                                                                          301 CACAACCGCGTGTGCGAATGCAAGGAAGGCGCGTACCTTGAGATAGAGTTCTGCTTGAAA
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            cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa
                                                                                                                          361 CATAGGAGCTGCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGGGAAATACA
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                                                                                                                                                                                                                                                         541 cacgacaacatatgttccggaaacagtgaatcaactcaaaaaatgtggaatagatgttacc
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                                                                                                                                                      gtttgcaaaagatgtccagatgggttcttctcaaatgagacgtcatctaaagcaccctgt
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding osteoclastogenesis inhibitory factor protein for bone resorption control, esp. treatment of osteoporosis Claim 36; Page 135-136; 183pp; Japanese.
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a M, Yano
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Ueda M,
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1..63
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LT
GCLO M, Higashlo K, Kobayashi F,
Nakagawa N, Shima N, Tsuda E, Ue
WPI; 96-402320/40.
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/product= OCIF-C22S
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C22S in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Ostebclastogenesis inhibitory factor coding sequence.
Ostebclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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20-FEB-1995, J00374.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M. Higashio K. Kobayashi F. Mochizuki S. Morinaga T;
Nakagawa N. Shima N. Tsuda E. Ueda M. Yano K, Yasuda H;
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841 gtgcagcggcacattggacatgctaacctca
                                 841 GTGCAGCGCACATTGGACATGCTAACCTCA
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T366<sub>8</sub>5 standard; DNA; 1206 BP
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P-PSDB; R99924-25
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/label= Claim 6
WO9626217-A1.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 39; Page 136-137; 183pp; Japanese This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C23S in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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Mutated OCIF, OCIF-C23S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
361 CATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGGAAATACA 420
                                                                                                                                                                                                                                                                   601 ctgtgtgaggaggcattcttcaggtttgctgttcctacaaagtttacgcctaactggctt 660
                                                                                                                                                                                                                                                                                                                                            661 agtgtcttggtagacaatttgcctggcaccaaagtaaacgcagagagtgtagagagata 720
                                                                                                                                                                                                                                                                                                                                                                  721 aaacggcaacacagctcacaagaacagactttccagctgctgaagttatggaaacatcaa 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deg.C. ÓCIF is useful in the control of bone resorption and therefor in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                           541 CACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACC
                                                                                                                                                                                                                                                                                                         CTGTGTGAGGAGGCATTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAAACTGGCTT
                                     421 GTTTGCAAAAGATGTCCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGT
                                                                                                                                                                                            cacgacaacatatgttccggaaacagtgaatcaactcaaaaatgtggaatagatgttacc
                                                                                                              481 agaaaacacacaaattgcagtgtctttggtctcctgctaactcagaaaggaaatgcaaca
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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WO9626217-A1.
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P-PSDB; R99935
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Mutated OCIF, OCIF-C20S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                          1 atgaacaacttgctgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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0
                         Length 1206;
                                                  2; Indels
268 G;
                         Score 867; DB 27;
Pred. No. 0.00e+00;
                                                   0; Mismatches
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285 C;
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389 A;
                          79.68;
99.88;
                                       Best Local Similarity 99.8%;
Matches 869; Conservative
1206 BP;
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                          Query Match
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 30; Page 133-134; 183pp; Japaneses.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C20S in which the 20th Cys residue in the mature ociF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its extivity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.4%; Score 865; DB 28; Length 1206; Best Local Similarity 99.7%; Pred. No. 0.00e+00; Matches 868; Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yasuda H;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNW) SNOW BRAND MILK PROD CO LTD.
GOCD M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
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                                                                Location/Qualifiers
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P-PSDB; R99932.
       osteoporosis; ss.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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RESULT 11

ID 713161 standard; DNA; 1206 BP.

AC 73161;

DT 22-APR-1997 (first entry)

EMUSTAGO OFF: VOIF-C195, coding sequence.

KW Osteoclastogenesis Inhibitory factor; OCIF; heparin; bone resorption; KW Asteoclastogenesis Inhibitory factor; OCIF; heparin; bone resorption; FT Asteoclastogenesis Inhibitory factor; OCIF; heparin; FT Asteoclastogenesis Inhibitor; Inhibitor; Inhibitor; Inhi
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 27, Page 132; 183pp; Japanese.
This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C19S in which the 19th Cys residue in the mature ocif protein is substituted by Ser. The OCIF of the invention has molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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Yasuda H;
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29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
P-PSDB; R99931.
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for bone resorption control, esp. treatment of osteoporosis claim 57; Page 142-143; 183pp; Japanese.
This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD2 in which amino acids 233-326 of the mature protein have been deleted. The OCIF of the invention has a molecular protein have been deleted. The OCIF of the invention has a molecular neight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under neducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 984 BP; 313 A; 236 C; 212 G; 223 T;
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                                                                                                                                                                                                                                                                                                                                                               22-ApR-1997 (first entry)
Mutated OCIF, OCIF-DDD2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
aacaaagaccaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 atgaacaacttgctgtgctgcgcgctcgtgttctggacatctccattaagtggaccacc 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 984;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 74.9%; Score 816; DB 27; Local Similarity 99.9%; Pred. No. 0.00e+00; les 817; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                    841 gtgcagcggcacattggacatgctaacctca 871
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T33171 standard; DNA; 984 BP.
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/product= OCIF-DDD2
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Mutated OCIF, OCIF-CDD2, coding sequence.
Osteochlastogenesis inhibitory factor; OCIF; heparin; bone resorption;
301 CACAACCGCGTGTGCGAATGCAAGGAAGGCCGCTACCTTGAGATAGAGTTCTGCTTGAAA
                                                                                                                                                    cataggagctgcctcctggatttggagtggtgcaagctggaaccccagagcgaaataca
                                           ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA eqcoding osteoclastogenesis inhibitory factor protein - for bone resorption control, esp. treatment of osteoporosis Claim 65; Page 145; 183pp; Japanese.
This Sequence encodes a mutated version of the full length
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a M, Yano K,
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Nakagawa N, Shima N, Tsuda E, Ueda M,
WPI; 96-402320/40.
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UTL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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T33174 standard; DNA; 819 BP.
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WO9626217-A1.
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P-PSDB; R99944
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sequence encodes OCIF-CDD2 in which amino acids 252-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 KD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 819 BP; 251 A; 198 C; 188 G; 182 T;
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                                                                                                                                                                                                             Length 819;
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Pred. No. 0.00e+00;
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99.98;
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Best Local Similarity 99.9%;
Matches 815; Conservative
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JT 14 T33166 standard; DNA; 1083 BP

RESULT

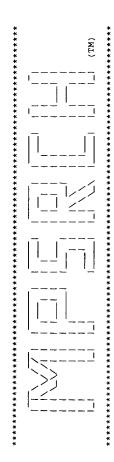
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181 gtgtgcgccccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240
  gtagacaatttgcctggcaccaaagtaaacgcagagagtgtagagaggataaaacggcaa
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                                                                                                                                                          727 cacattggacatgctaacctca 748
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T33170 standard; DNA; 981 BP.
T33170;
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                                                                                                                                                                                                                                                                                        DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 42; Page 137-138; 183pp. Japanese.

This sequence encodes mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DCR1 in which amino acids 2-42 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.

Sequence 1083 BP; 352 A; 250 C; 246 G; 235 T;
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           22-APR-1997 (first entry)
Mutated ocIF, OCIF-DCR1, coding sequence.
OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
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                                                                                                                                                                                                                                                       Yasuda H;
                                                                                                                                                                                               20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa M, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 682; DB 27;
Pred. No. 0.00e+00;
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                                                                      Location/Qualifiers
1..63
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Local Similarity 100.0%;
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20-FEB-1996; J00374
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mat_peptide
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for bone resorption control, esp. treatment of osteoporosis
Claim 54; Page 141-142; 183pp; Japanese.
This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD1 in which amino acids 178-252 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and
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670 GTAGACAATTTGCCTGGCACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAA 729
                                                                                                                caagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagcgtgcagcgg 726
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Mutated OCIF: OCIF-DDD1, coding sequence.
OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
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                                                                                cacagetcacaagaacagaetttecagetgetgaagttatggaaacatcaaaaeaaagae
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20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
NAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 3 10:06:20 1997; MasPar time 2.51 Seconds 29:342 Million cell updates/sec

bular output not generated.

Cle: >US-08-915-004-1 Description: (1-6) from US08915004.pep Perfect Score: 47

Sequence: 1 XYHFPK 6

Scoring table: PAM 150 Gap 15 Searched: 101610 seqs, 12294212 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq28

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21

Statistics: Mean 14.688; Variance 38.315; scale 0.383

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ilt Mo	Score	Query	Length	DB	ID	Description	Pred. No.
7	47	100.0	9	20	R99921	Osteoclastogenesis in	2.01e+01
2	47	100.0	326	20	R99940	Mutated OCIF, OCIF-DD	2.01e+01
е	47	100.0	327	20	R99941	Mutated OCIF, OCIF-DD	2.01e+01
4	47	100.0	359	20	R99939	Mutated OCIF, OCIF-DC	2.01e+01
S	47	100.0	359	20	R99937	_	2.01e+01
9	47	100.0	360	20	R99938	Mutated OCIF, OCIF-DC	2.01e+01
7	47	100.0	360	20	R99936	Mutated OCIF, OCIF-DC	2.01e+01
æ	47	100.0	380	20	R99924	Mature osteoclastogen	2.01e+01
6	47	100.0	393	20	R99948	Mutated OCIF, OCIF-CB	2.01e+01
10	47	100.0	399	20	R99942		2.01e+01
11	47	100.0	401	20	R99935		2.01e+01
12	47	100.0	401	20	R99932	Mutated OCIF, OCIF-C2	2.01e+01
13	47	100.0	401	20	R99931	Ξ.	2.01e+01
14	47	100.0	401	20	R99934	Mutated OCIF, OCIF-C2	2.01e+01
15	47	100.0	401	20	R99933	Mutated OCIF, OCIF-C2	2.01e+01
16	47	100.0	401	20	R99925	Full length osteoclas	2.01e+01
17	43	91.5	505	-	P81265	Sequence encoded by p	6.35e+01
18	42	89.4	1137	15	R90766	Tumour suppressor pro	8.43e+01
19	40	85.1	188	12	R66461	AF-17 protein, N-term	1.47e+02
20	40	85	255	4	R23005	Protein transcribed f	1 470+02

1.47e+02 1.47e+02 1.47e+02 1.47e+02	1.47e+02 1.47e+02 1.47e+02 1.47e+02	1.47e+02 1.47e+02 1.47e+02	1.47e+02 1.47e+02 1.47e+02	1.47e+02 1.47e+02 1.47e+02 1.47e+02	
necrosi 14-hydr nifera in-like	Soluble human IGF-I r Extracellular domain Hybrid human insulin- Human contactin.		recep	Human type I insulin- Human type I insulin- IGF-I receptor. IGF-I receptor.	Trotal pain lar pylori s eromonas lence en
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ALIGNMENTS

SUL	N 899921 standard; peptide; 6 AA. R 899921;		Osteoclastogenesis inhibitory factor peptide fragment #1.		ostec	Homo sapiens.				_	29-AUG-1996.	20-FEB-1996;	20-FEB-1995;	21-JU	(SNOW) SNOW BRAND MILK PROD CO LTD.	Goto M, Higashio K, Kobayashi F, Mochizuki		WPI;	DNA		Clai		the	The OCIF has a molecular weight by SDS-PAGE of 60 kD u		adsorbed onto cation-exchangers or heparin and its	lowered after 10 mins at 70 deg.C or 30 mins at 56	lost after 10 mins at 90 deg.C. OCIF is useful in		disorders	2 Sequence o AA;	
RE	R B	ΔŢ	DE	X	Ϋ́	os	FH	F	F	ď	B	PF	PR	PR	PA	PI	Ы	DR	PT	ЬŢ	D.	ပ	႘	ပ	ပ္ပ	႘	ပ္ပ	ပ	ပ္ပ	ပ္ပ	Ŋ	

Query Match 100.0%; Score 47; DB 20; Length 6; Best Local Similarity 100.0%; Pred. No. 2.01e+01; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

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RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for pure forecolastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis.

This page 113-114; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoporasis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD1 in which amino acids 178-252 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the contion of disorders of bone resorption, e.g.
                   23-ApR-1997 (first entry)
Mutated OCIF, OCIF-DDD1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
Osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutated OCIF, OCIF-DDD2. OS (Sector) OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 20; Length 326; Pred. No. 2.01e+01; 0; Mismatches 0; Indels
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W096404...
W096404...
W0-FEB-1996; J00374...
W1-1995; JP-054977...
W1-1995; JP-207508...
WNOW BRAND MILK PROD CO LTD...
Higashio K, Kobayashi F, Mochizuki S,
                                                                                                                                                                                                                                                                                                                                 20-FB-1996; J00374.
20-FB-1996; JP-054977.
21-JUL-1995; JP-054977.
SNOW JS NOW BRAND MILK PROD CO LTD.
Goto | M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 196-402320/40.
                                                                                                                                                                                                           Protéin 22..326
/noté= "Mature COIF-DDD1"
/noté= "Positition of deletion, delta 178-252"
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Protein 22.327
/note "Mature OGIF-DDD2"
/note "Positition of deletion, delta 253-326"
                                                                                                                                                Location/Qualifiers
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R99940 standard; Protein; 326 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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W09626217-Al.
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                                                                                                                              Synthetic.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 59; Page 115-116; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 253-326 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. ocif is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Claim 53: Page 111-113; 183pp; Japanese.
This sequence represents a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence represents OCIF-DCR4 in which amino acids 123-164 of the
mature OCIF protein are deleted. The OCIF of the invention
has a molecular weight by SDS-PAGE of 60 Bounder reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins
at 70 deg.C. OCIF is useful in the control of bone resorption and therefore
in the treatment and prevention of disorders of bone resorption, e.g.
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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1...1

Prote Signal peptide 22...359

/note Wature OCIF-DCR4 / Mosc_difference 143...144 / Mosc_ Post fittion of deletion, delta 123-164*
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Best Local Similarity 100.0%;
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Matches 5; Conservative
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for bone resorption control, esp. treatment for osteoporosis

Claim 47; Page 107-109; 183pp; Japanese.

This sequence represents a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence represents OCIF-DCR2 in which amino acids 43-84 of the
mature OCIF protein are deleted. The OCIF of the invention
has a molecular weight by SDS-PAGE of 60 bunder reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins
at 70 deg.C. OCIF is useful in the control of bone resorption and therefore
                                                                     Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 20; Length 359;
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0; Mismatches 0; Indels
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20-FEB-1995; JP-05497.
21-071-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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Misc_difference 105..106
/note= "Position of deletion, delta 85-122"
                                                                                                                                                             Protein 22..359
/note= "Mature OCIF-DCR2"
Misc_difference 63..64
/note= "Position of deletion, delta 43-84"
                                                                                                                       Location/Qualifiers
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7 5
R99937 standard; Protein; 359 AA.
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R99938 standard; Protein; 360 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                          23-APR-1997 (first entry) Mutated OCIF, OCIF-DCR2.
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                                                                                                                                                  /note= "Signal peptide"
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20-FEB-1995; JP-05497
21-JUL-1995; JP-20750
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                             R99937;
                                                                                                                                  Peptide
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Gaps

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NA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 50. Page 109-111; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or hepzin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-DCR1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
                                          Morinaga T
Yasuda H;
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
N-PSDB; T33168.
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/note= "Position of deletion, delta 2-42"
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Score 47; DB 20; Length 360; Pred. No. 2.01e+01;

Query Match Best Local Similarity 100.0%;

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2 YHFPK 6
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                                                                                                                                                                                               22-APR-1997 (first entry) Mature osteoclastogenesis inhibitory factor. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 6; Page 62-64; 183pp; Japanese.
This sequence represents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE 0f 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
Gaps
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Yasuda H;
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Yasuda H;
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
  Indels
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20-FEB-1996; JP-054977.
21-JUL-1995; JP-054977.
SNOW BRAND MILK PROD CO LTD.
GCto M. Higashio K. Kobayashi F. Mochizuki S,
Nakagawa N. Shima N. Tsuda E. Ueda M. Yano K,
WPI: 96-402320/40.
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; T33178.
0; Mismatches
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                                                                                                                                                                  R99924 standard; Protein; 380 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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/note= "Mature OCIF-CBst"
Misc_difference 392
/label= Gln371Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1997 (first entry)
Mutaled OCIF, OCIF-CBSt.
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  5; Conservative
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/note= "Signal peptide"
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                                         314 yhfpk 318
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WO9626217-A1.
29-AŬG-1996.
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                                                                 2 XHFPK 6
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Matches
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 80; Page 126-128; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-Cabst in which Gln 371 is substituted by cleu and amino acids 373-380 of the mature OCIF protein are deleted. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the creatment and prevention of disorders of bone resorption, e.g.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CL in which amino acids 379-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LID.
GOLO M, Highshio K, Kobayashi F, Mochizuki S, Morinaga T;
Wakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
WPI: 96-402320/40.
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100.0%; Score 47; DB 20; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.01e+01;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 20; Length 393;
Pred. No. 2.01e+01;
0; Mismatches 0; Indels
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R99942 standard; Protein; 399 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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/note= "Signal peptide"
Protein 22..399
/note= "Mature OCIF-CL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA;
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RESULT

US-08-915-004-1.rag

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis.

Idaim 32. Page 96-98; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or hepzin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Laim 29. Page 94-96; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents offer-C19s in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto extion-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of sorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1997 (first entry)
Mutated OCIF, OCIF-C19S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
      Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 20; Length 4U1;
Pred. No. 2.010+01;
''...ma+rhes 0; Indels
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20-AUG-1996
20-FEB-1995; JP-054977.
20-FEB-1995; JP-054977.
21-JUL-1995; JF-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOTO M, H1gashio K, Kobayashi F, Mochizuki S, Mc
WPL; 96-402320/40.
N-PSDB; T33161.
    F, Mochizuki S,
Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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    Kobayashi
Tsuda E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 100.0%;
Local Similarity 100.0%;
les 5; Conservative
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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/note= "Mature OCIF-C198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide 1..21
/note= "Signal peptide"
Goto M, Higashio K, Nakagawa N, Shima N, WPI; 96-402320/40. N-PSDB; T33162.
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/label= C19S
                                                                                                                                                                                                                                                                                                                                                                              401 AA;
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                                                                                                                                                                                                                                                                                                                                                             osteoporosis
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C23S in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 Mo under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of eg.
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                                                                                                                     Mutated OCIF, OCIF-C23S. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Mutated OCIF, OCIF-C20S.
Osteoporosis, inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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Pred. No. 2.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 29-400-1996.
20-FBB-1996. JO0374.
20-FBB-1995. JP-054977.
21-001-1995. JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; Ţ33165.
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                         Location/Qualifiers
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                                    .m. 11
R99935 standard, Protein, 401 AA.
R99935;
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                                                                                                                                                                                                                      Peptide | 1..21

/note= "Signal peptide" | 22.401

/note= "Mature OCIF-C23S" | Misc_difference 400 | 7.1abel= C23S | W09626217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                 22-APR-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 yhfpk 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- C20S
W09626217-A1.
                                                                                                                                                            osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis
                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R99932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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Gaps

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Score 47; DB 20; Length 401; Pred. No. 2.01e+01;
                         0; Indels
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Morinaga T; Yasuda H;

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20-FEB-1995; JP-054977.
21-JUL-1995; JP-054977.
6SNOW DRAND MILK PROD CO LTD.
GOTO M, Higashio K, Kobayashi F, Mochizuki S, Nakagwa M, Shima N, Tsuda E, Ueda M, Yano K, WPI: 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R99925 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein 22..401
/note= "Mature OCIF, claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide 1..../
/note= "Signal peptide" 401
20-FEB-1996; J00374.
                                                                                                                                                                                                                                                                                                                                            401 AA;
                                                                                                         N-PSDB; T33163.
                                                                                                                                                                                                                                                                                                                                                                                                                                        355 yhfpk 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis
                                                                                                                                                                                                                                                                                                                                osteoporosis
                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 38, Page 100-102, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22S in which the 27nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutated OCIF, OCIF-C21S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                   Mutared OCIF, OCIF-C22S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dery Match 100.0%; Score 47; DB 20; Length 401; set_Local Similarity 100.0%; Pred. No. 2.01e+01; Indels
                                                                                                                                                                                                                                                                                                         /label= C225

W09626217-A1.

20-406-1996.

20-FEB-1995. JP-054977.

20-FEB-1995. JP-054977.

21-JUL-1995. JP-057508.

(SNOW) SNOW BRAND MILK PROD CO LTD.

GOto |M. Higashio K, Kobayashi F, Mochizuki S, Mo

Nakadawa N, Shima N, Tsuda E, Ueda M, Yano K, Ya

NPI: 96-402320/40.
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                          T 114
R99934 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R99933 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide 1..21

/note= "Signal peptide"

Protein 22..401

/note= "Mature OCIF-C21S"

Misc_difference 277

/label= C21S

W09656217-A1.

29-AUG-1996.
                                                                                                                         R99934;
22-APR-1997 (first entry)
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                                                                                                                                                                                                                                                             Protein 22.401
/note= "Mature OCIF-C228"
Misc_difference 277
                                                                                                                                                                                                                                               "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 AA;
             355 yhfpk 359
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                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                 Peptide
/note= "s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Note that the conding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 35; Page 99-100; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C21S in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Disclosure; Page 64-66, 183pp, Japanese.

This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1997 (first entry)
Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 47; DB 20; Length 401; Best Local Similarity 100.0%; Pred. No. 2.01e+01; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 20; Length 4vi,
Pred. No. 2.010+01;
......+rhes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 401;
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20-FEB-1996; J00374.
20-FEB-1995; JP-02497.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Waragawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; T36685.
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New virulence plasmid pkDSC50 - provides DNA fragment useful as probe for detecting Salmonella Disclosure; Fig 2: ppp; Japanes Disclosure; Fig 2: ppp; Japanes Fig 2: ppp; Tapanes Fig 2: protein may be transcribed from the second reading frame of the "mba" fragment of virulent plasmid pkDSC50 from nucleotides 2564-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis and treatment of leukaemias, partic, acute lymphoblastic or nonlymphoblastic leukaemia Calaim 53; Page 134-135; 207pp; English.
Monoclonal antibodies which bind to at least part of the chimeric ALL-L/AR-17 protein (R66450) or to part of the AR-17 protein (see R66460 and R66461) are claimed. The antibodies are useful for diagnosing acute lymphoblastic and non-lymphoblastic leukaemia.
                                                                                                                                                                                                                                                   AF-17 protein, N-terminal region with similarity to peregrin. Acute lymphoblastic leukaemia, chromosomal translocation, abnormality, detection; chimeric ALL-1/AF-17 protein; ALL-1 fused gene on chromosome 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R23005;
29-OCT-1992 (first entry)
Protein transcribed from the mba sequence of plasmid pKDSC50.
Virulent; Salmonella choleraesuis; mouse bacteremia; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canaani E, Croce C;
WPI; 95-006818/01.
New acute lymphocytic leukaemia gene prods. - used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "region of 90% identity to anonymous human
cDNA sequence (Genbank Acc.No.To6113)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 12; 1
Pred. No. 1.47e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "cysteine-rich region with similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0942052.
24 NOV-1994.
22 APR-1994; U04496.
14 MAY-1993; US-065443.
4 (UVJE-) UNIV JEFFERSON THOMAS.
5 Croce C; Croce C;
                                                                                                                                                                  R66461 standard; Protein; 188 AA.
R66461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .T 20
R23005 standard; Protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-1990; 194069.
24-JUL-1990: JP-194069.
(KIBU-) KIBUN KK.
(KITA ) KITASATO RES INST.
WPI; 92-137918/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0%;
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120..140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label = zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= zinc-finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peregrin protein"
720 yqfpk 724
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                                   |:|||
2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                           24-AUG-1995
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27-JAN-1988.
28-JAN-1988.
28-JUL-1986; FR-010829.
28-JUL-1986; FR-010829.
28-JUL-1986; FR-010829.
29-JAN-1989.
29-JAN-1989.
29-JAN-1989.
20-JAN-1989.
20-JAN-1988.
20-JAN-1988
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                                                                                                                                                                                                                                       12-DEC-1990 (first entry)
Sequence encoded by part of AAC(6')-APH(2'') (6'-acetlytransferase-2''-
phosphotransferase) gene in the plasmid pIP800 of Streptococcus
faecalis JH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour suppressor gene, HTS-1 - shows differential expression in tumorigenic and normal cells and may be useful in tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prognosis
Column 19-26; 17pp; English.
Human tumour suppressor protein HTS-1 (R90766) is produced by
Procaryotic or eucaryotic host cells transformed or transfected by
Procaryotic or elcaryotic host cells transformed or transfected by
a vector including an isolated HTS-1 cDNA (T12473). Expression of
a vector including an isolated HTS-1 cDNA (T12473).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTS-1 is associated with tumour suppression. The purified HTS-1 protein can be used to raise antibodies for use in HTS-1 detection. Sequence 1137 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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Tumour suppressor protein HTS-1.
Tumour suppressor protein; HTS-1; cancer; therapy; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                        gentamycin resistant; Staphylococcus; antibiotic resistant. Streptococcus faecalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 1; Length 505; Pred. No. 6.35e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                             Streptococcal plasmid pGB3012; kanamycin resistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 15; 1 Pred. No. 8.43e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-1996.
17-JUL-1992, 916762.
17-JUL-1992, US-916762.
05-JAN-1995, US-369043.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
HOWLEY PM, LICHY JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R90766 standard; Protein; 1137 AA
                                                                                                                                                                                    P81265 standard; protein; 505 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.5%;
80.0%;
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ilarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ey PM, Lichy JH;
96-116319/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                 355 yhfpk 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 yhypk 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
US5491064-A.
                                                                    2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                             FR2601965-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Gaps

US-08-915-004-1.rag

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Three other proteins may also be transcribed from the Salmonella
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The receptor binds to TNF, and in particular, TNF-beta.

The receptor may be used for screening for antigonists and agonists of the receptor may be used for screening for antigonists and agonists be used to inhibit the growth of tumours, to stimulate cellular differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapecutically, to treat auto-immune diseases, inflammation, septic shock, to inhibit graft-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-1997 (first entry)
Daunofrubicin 14-hydroxylase.
darA; doxorubicin: biocorubersion; anthracycline; antitumour therapy;
daunofrubicin 14-hydroxylase.
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour necrosis factor receptor.
Tumour necrosis facor; INF; receptor; INF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
                                                                                                                                                                                                                          ;
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0
   "mba" fragment, which is capable of causing mouse bacteremia. See also R23004-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 20; Length 390;
Pred. No. 1.47e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-1996.
27-FEB-1995; BO0692.
27-FEB-1995; UG-396218.
(PHAA) PHARMACIA SPA.
Breme U, Colombo AL, Hutchinson CR, Otten S, Scotti C;
                                                                                                                               Score 40; DB 4; Lengtn 20, Pred. No. 1.47e+02; ....matrhes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 versus-host reactions, and to prevent apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             septic shock; graft-versus-host; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces peucetius strain 29050. WO9627014-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W00729 standard; Protein; 422 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 21
R9935/7 standard; Protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MA'Y-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= sig_peptide
W09628546-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleischmann RD, Gr
WPI; 96-433821/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T35475.
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                                                                                                                                                                                                                                                                                       yhfp 138
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                                                                                              Sequence
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                                                                                                                                                                                                                                                                                          135
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claim 4; Page 15-18; 31pp; English.

The present sequence is that of the daunorubicin 14-hydroxylase, isolated from Streptomyces peucetius strain 29050. The enzyme converts daunorubicin to doxorubicin, an anthracycline used widely as an antitumour agent. A vector contg. the drxA gene (733617) could be used to transform a suitable host cell which produces daunorubicin, in order to enhance bioconversion of daunorubicin to doxorubicin. Bioconversion can be carried out either by using directly the free or immobilised transformed cells or by isolating the enzyme, which can be used in the free form or immobilised to resins, glass, cellulose or similar substances by ionic or covalent bonds, or graffed to fibres permeable to the substrate or insolubilised by cross-linkage.
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WPI; 96-151378/15.

The continuation of fumonisin and related mycotoxin cpds. in grains response esp. an esterase, from Exophiala spinifera, which an enzyme esp. are abacterium Example 8; Pages 33-34; 54pp; English.

Example 8; Pages 33-34; 54pp; English.

The present sequence is the Exophiala spinifera (ATCC 74269) fumonisin esterase, which was isolated from a maize seed. The gene which encodes the esterase can be used to produce transgenic plants and genetically engineered microorganisms, capable of expressing the esterase. The microorganisms can be used as a problotic or feed inoculant, along with the esterase to degrade fumonisins and related cpds., partic. for the detoxification of maize seed pre- or post-harvest (i.e. during the storage or processing of the harvested grain, or in the processed grain)
Solari INVENTI A, Inventi AS;
WPI; 96-412780/41.
N-PSDB; 713617.
New DNA encoding daunorubicin 14-hydroxylase - useful for converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exophiala spinifera fumonisin esterase.

Fumonisin; esterase; transgenic plant; recombinant microorganism; expression; probiotic; feed inoculant; degradation; detoxification; maize seed; grain; animal feed.

Exophiala spinifera.
                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 19; Length 422;
                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 18; Length 52/
Pred. No. 1.47e+02;
.............0; Indels
                                                                           daunorubicin to the antitumour agent doxorubicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IT 24
R14402 standard; Protein; 934 AA.
R14402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R91277 standard; Protein; 527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1994; US-289595.
07-UUN-1995; US-484815.
(PION-) PIONEER HI-BRED INT INC.
DUVICK J, ROOD TA;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative
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Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-FEB-1996.
11-AUG-1995; U10284.
                                                                                                                                                                                                                                                                                                                                    422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                156 yhfp 159
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ID R1
AC R1
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75 yrfpk 79

g

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including exons from two separate receptors, having improved growth performance in serum-free medium bisclosure: Fig 3: 57pp; English.

The amino acid sequence is that of the soluble insulin-like growth factor (IGF) receptor. It is used here as part of a fusion protein produced by a hybrid DNA insert comprising a DNA sequence encoding part of the extracellular domain of the IR and a sequence coding for part of the ECD of an insulin like growth factor (IGF). Cells contg. this insert have better growth characteristics in both serum-contg. and partic. Serum-free media. This makes them useful for expressing polypeptides (e.g. human blood clotting factors; tissue plasminogen activator; human protein C), encoded by a third DNA sequence. The polypeptides of an now be purified more easily and produced in better yield. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybrid cellular receptor - has 2 sequences encoding extracellular domain of receptors having different ligand binding extracellular domain of receptors having different ligand binding extracellular domain of receptors having different ligand binding Example 1; Fig 4; 97pp; English.

Example 1; Fig 4; 97pp; English.

The sequence was deduced from a cDNA sequence prepd. from mRNA isolated from human term placenta by PCR amplification. The full sequence was assembled from four subcloned fragments and was found to be identical to that published by Ullrich et al (The EMBO Ordinal 5(120), 1986, pp 2503-2512). The DNA can be ligated to DNA encoding a sol. insulin receptor (see Q14813) to prepare hybrid proteins. The new receptors are useful for screening for ligands of proteins. The new receptors are useful for screening for ligands for scalishing the 3-D structure of the ligand binding site and for designing analogues or functional equivalents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                               Mammalian cells contg. hybrid DNA for extracellular receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 3; Length 934; Pred. No. 1.47e+02; 1; Mismatches 0; Indels
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Pred. No. 1.47e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kjeldsen T, Andersen AS, Wiberg F, Moller N, Rasmussen J;
WPI; 91-353773/48.
N-PSDB; Q14814.
                                                                                                                                                     14-NOV-1991.
30-APR-1991. DK0116.
30-APR-1991. DK-001064.
(NOVO ) NOVO NORDISK A/S.
Wiberg FC, Olsen F, Boel E, Kjeldsen TB, Moller NPH.
WPI; 91-353774/48.
14-FEB-1992 (first entry)
Soluble Insulin-like Growth Factor receptor.
Extracellular receptor; IGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R15048 standard; Protein; 934 AA.
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14-FEB-1992 (first entry)
Soluble human IGF-I receptor.
Insulin-like growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.1%;
llarity 80.0%;
Conservative
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30-APR-1991; DK0115.
30-APR-1990; DK-001063.
03-AUG-1990; DK-001855.
(NOVO ) NOVO NORDISK A/S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also R15047-51.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             934 AA;
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N-PSDB; Q14380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 yrfpk 79
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WO9117252-A.
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Matches
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Gaps

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85.1%; 80.0%;

Local Similarity

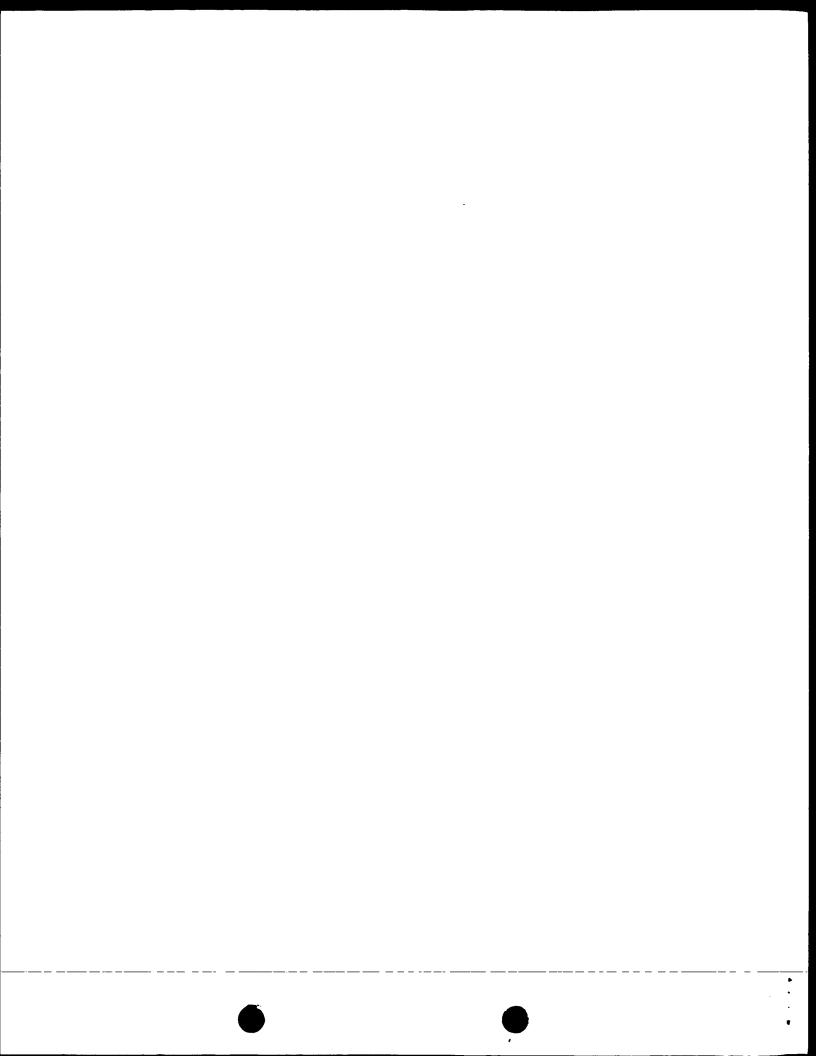
Best Loc Matches

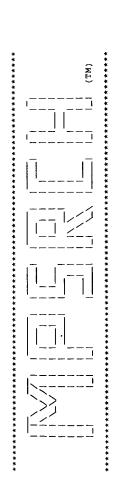
Query Match

4; Conservative

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Mammalian cells contg, hybrid DNA for extracellular receptor including exons from two separate receptors, having improved frow two separate receptors, having improved size the performance in serum-free medium disclosure; Fig 4: 57pp; English.

The amino acid sequence is that encoded by a hybrid DNA insert comprising a DNA sequence encoding part of the extracellular domain of the IR and a sequence coding for part of the extracellular domain of the IR and a sequence coding for part of the ECD of an insulin like growth factor (IGF). Cells contg, this insert have better growth characteristics in both serum-contg, and partic. serum-free media. This makes them useful for expressing polypeptides (e.g. human blood clotting factors; tissue plasminogen activator; human protein C), encoded by a third DNA sequence. The polypeptides can now be purified more easily and produced in better yield. See also R14402.
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                                                                                                                                                                                            14-FEB-1992 (first entry)
Extracellular domain of hybrid insulin/IGF-I receptor.
Extracellular receptor; IGF; fusion protein.
                                                                                                                                                                                                                                                                                                                             14-NOV-1991.
30-APR-1991; DK0116.
30-APR-1990; DK-001064.
(NOVO ) NOVO NORDER A/S.
Wiberg FC, Olsen F, Boel E, Kjeldsen TB, Moller NPH.
WPI; 91-353774/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: Wed Dec 3 10:06:32 1997 Job time: 12 secs.
                                                                                            .r 26
R14403 standard; Protein; 948 AA.
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Best Local Similarity 80.0%;
Matches 4; Conservative
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2 YHFPK 6
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2 YHFPK 6
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 2 14:43:12 1997; MasPar time 5.65 Seconds 30.699 Million cell updates/sec

ular output not generated.

-itle: >US-08-915-004-1
Description: (1-6) from US08915004.pep
Perfect Score: 47

Sequence: 1 XYHFPK 6 Scoring table: PAM 150 Gap 15 Searched: 91006 segs, 28888923 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir51

Statistics:

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev Mean 20.106; Variance 27.499; scale 0.731

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES		
sult No.	Score	* Query Match	Length	DB	ΙD	Description	Pred. No.
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7	47	100.0	562	14	B56101	collagen alpha 1(XVI	4.96e+00
e	43	91.5	479	σ	A26048	coside	2.88e+01
4	43	91.5	479	σ	S26353	aminoglycoside resis	2.88e+01
S	43	91.5	803	14	A41793	dipeptidyl aminopept	2.88e+01
9	43	91.5	803	13	168600	dipeptidyl aminopept	2.88e+01
7	43	91.5	865	13	154331	dipeptidyl aminopept	2.88e+01
ω	43	91.5	-	Ξ	S32613	HEX2 protein - yeast	2.88e+01
σ	42	89.4	-	Н	S58182	nonstructural protei	4.41e+01
10	42	89.4		٦	S58186	nonstructural protei	4.41e+01
11	42	89.4		16	S58184	nonstructural protei	4.41e+01
12	42	89.4		4	A44275	nonstructural protei	4.41e+01
13	42	89.4		12	S42791	PES-1B protein - Cae	4.41e+01
14	42	89.4		12	S42793	PES-1 protein - Caen	4.41e+01
15	42	89.4		σ	A47092	replication protein	4.41e+01
16	42	89.4	349	16	S65928	hypothetical protein	4.41e+01
17	42	89.4	٣	11	S52763	hypothetical protein	4.41e+01
18	42	89.4		П	A49013	HTS1 - human (fragme	4.41e+01
19	42	89.4	7	٦	S23353	gene unc-93 protein	4.41e+01
20	42	89.4	705	٦	523352	gene unc-93 protein	4.41e+01
21	42	89.4	1511	12	S60932	probable membrane pr	4.41e+01

	6.70e+01	1.01e+02	1.01e+02	1.01e+02		1.01e+02	1.01e+02			1.01e+02	1.01e+02	1.01e+02		1.01e+02		•	1.01e+02	•	1.01e+02	•	1.01e+02	1.01e+02	1.01e+02	
S					hypothetical protein	36K protein - Achole	matrix protein - Sen	matrix protein - Sen	rbfB homolog - Xanth	hypothetical protein	se se	rfbB protein - Shige	rfbB protein - Salmo	major early-transcri	deoxyribodipyrimidin	nuclear protein SON1	penicillin-binding p	phosphoprotein phosp	neuronal cell surfac	contactin precursor	mRNA guanylyltransfe	insulin-like growth	insulin-like growth	
139731	B32053	S22627	S62589	IKECM	S46770	B42653	MFNZS	MFNZSV	B49906	E64023	I55054	B55213	S15299	A45709	S00757	S41986	A55220	PABY12	S05944	A57112	RMXRR3	IGHUR1	A33837	
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238	252	113	209	271	283	327	348	348	351	353	361	361	361	449	484	531	624	692	1020	1021	α	36	1371	
	87.2	85.1	'n	85.1	85.1	'n.	'n	85.1	ď.	'n.	'n.	85.1	'n	85.1	D	85.1	'n	S	S	85.1	85.1	85.1	85.1	
41	41	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	
22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45	

ALIGNMENTS

A56101 #type fragment collagen alpha 1(XVIII) chain precursor short form - mouse (fragment) (fragment) 03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change	A550101 Rehn, M.; Pihlajaniemi, T. Rehn, M.; Pihlajaniemi, T. J. Biol. Chem. (1995) 270:4705-4711 Identification of three N-terminal ends of type XVIII collagen chains and tissue-specific differences in the expression of the corresponding transcripts. The longest form contains a novel motif homologous to rat and Drosophila frizzled proteins.	cession A56101 ##status preliminary ##status preliminary ##residues 1.103 ##label REH ##cross-references GB:U11636 CS COL18A1 references TB COL18A1 references TB COL18A1	Similarity 100.0%; Score 47; DB 14; Length 103; Similarity 100.0%; Pred. No. 4.96e+00; S. Conservative 0; Mismatches 0; Indels 0; Gaps 0; pk 78 1 1 1 1 1 1 1 1 1	#type fragment collagen alpha 1(XVIII) chain precursor long form - mouse (fragment) #formal_name Mus musculus #common_name house mouse #formal_name Mus musculus #common_name house mouse 03-0ct-1995 ##cort-1995 ##cort-19
A56101 collag (fra #forma 03-Oct	A56101 A56101 Rehn, J. Bio Identi coll expr form	ASSIGITY Pre Ltype mRN 1-1 ferences COL18A1	ilarity Conse 78 6	B56101 collade (frac #formal 03-Oct- 03-Oct- B56101 A56101 Rehn, b
RESULT 1 ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors #journal #title	#accession A55101 ##status ##molecule_type mRNA ##residues 1-10 ##cross_references G GENETICS COL18A1 #gene COL18A1 SUMMARY #length 1	Ouery Match Best Local Simi Matches 5; Db 74 yhfpk 7	RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #journal

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\#\# cross\mbox{-references EMBL:}M18086 \#\# note the authors translated the codon GAT for residue 374 as
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Best Local Similarity 80.0%;
Matches 4; Conservative
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J. Gen. Microbiol. (1987) 133:3039-3052
The aacA-aphD gentramicin and kanamycin resistance determinant
of In4001 from Staphylococcus aureus: expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $26353  #type complete aminoglycoside resistance protein aacA-aphD - Staphylococcus aureus transposon Th4001  #formal_name Staphylococcus aureus  #formal_name Staphylococcus aureus  03-May-1994  #sequence_revision 20-Feb-1995  #text_change
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Identification of three N-terminal ends of type XVIII collagen chains and tissue-specific differences in the expression of the corresponding transcripts. The longest form contains a novel motif homologous to rat and Drosophila frizzled proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Ferretti, J.J.; Gilmore, K.S.; Courvalin, P.
#journal J. Bacteriol. (1986) 167.631-638
#title Nucleotide sequence analysis of the gene specifying the bifunctional 6'-aminoglycoside acetyltransferase 2"-aminoglycoside phosphotransferase enzyme in Streptococcus faecalis and identification and cloning of gene regions specifying the two activities.
#cross_references MUID:86277923
#accession A26048
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aminoglycoside acetyltransferase - Enterococcus faecalis
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05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change
18-Jun-1993
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Pred. No. 4.96e+00;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                    ##molecule_type mRNA
##residues 1-562 ##label REH
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                                                                                                                                                                                            preliminary
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Shimasaki, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:197-201
#title Differential expression of two distinct forms of mRNA encoding members of a dipeptidyl aminopeptidase family.
#cross-references MUID:92108018
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#molecular-weight 56855 #checksum 5383
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#length 803 #molecular-weight 90459 #checksum 9315
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91.5%; Score 43; DB 14; Length 803;
Best Local Similarity 80.0%; Pred. No. 2.88e+01;
Matches 4; Conservative 1; Mismatches 0; Indels
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##molecule_type mRNA
                                                              Length 479;
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                                                        Score 43; DB 9; Le
Pred. No. 2.88e+01;
1; Mismatches 0;
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#journal Mol. Cell. Biol. (1992) 12:2673-2680

#title SRN1, a yeast gene involved in RNA processing, is identical to HEXX/REG1, a negative regulator in glucose repression.
#cross-references MUID:92269840
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HEX2 protein - yeast (Saccharomyces cerevisiae)
Protein D3402; protein P2F240; protein YD8013.06c; protein YD8028c; SRN1 protein #formal_name Saccharomyces cerevisiae
#formal_name Saccharomyces cerevisiae
30-Sep-1993  #sequence_revision 30-Sep-1993  #text_change
                                                                                                                                                                                                                                                                                                   #authors Yokotani, N.; Doi, K.; Wenthold, R.J.; Wada, K.
#journal Hum. Mol. Genet. (1993) 2:1037-1039
#title Non-conservation of a catalytic residue in a dipeptidyl
aminopeptidase IV-related protein encoded by a gene on
human chromosome 7.
#cross-references MUID:93372805
                                                                                                                                                             154331 #type complete
dipeptidyl aminopeptidase like protein - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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submitted to the EMBL Data Library, December 1992
S3261
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submitted to the EMBL Data Library, January 1994
S50935
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##residues 1-865 ##label RES
##cross-references GB:M96859; NID:9306705; CDS_PID:9306706

xx #length 865 #molecular-weight 97587 #checksum
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Pred. No. 2.88e+01;
1; Mismatches 0; Indels
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Pred. No. 2.88e+01;
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##molecule_type DNA
***~cidnes 962-1014 ##label TU2
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S32613
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##residues
##cross-references EMBL:247814
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##residues 1-1014 ##label TU1
##cross-references EMBL:M90540
                  Similarity 80.0%;
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Best Local Similarity 80.0%;
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honstructural protein, 12.8K - porcine hemagglutinating encephalomyelitis virus (strain 67N)
#formal_name porcine hemagglutinating encephalomyelitis virus
13.7an-1996 #sequence_revision 13.7an-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-375,'EE',378-533,'K',535-656,'H',658-888,'T',890-987,
'QEVWQASTCTLGKRVTSSHKKMEMTAVRRKNFEVN' ##label NI2
##cross-references EMBL:M33703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Eide, L.G.; Sander, C.; Prydz, H.
#authors Eide, L.G.; Sander, C.; Prydz, H.
#submission submitted to the EMBL Data Library, February 1996
#description Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV for Saccharomyces cerevisiae reveal 23
popen reading frames.
#accession S63438
##molecule_type DNA
##residues 775-1014 ##label EID
##cross-references EMBL:X95966
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'QEVWQASTCTLGKRVTSSHKKMEMTAVRRKNFEVN' ##label NIE
##cross-references EMBL:M33703
ENCE S27374
athors Niederacher, D.; Entian, K.D.
Danission submitted to the EMBL Data Library, April 1990
                                                    #duthors Niederacher, D.; Entian, K.D.
#journal Eur. J. Biochem. (1991) 200:311-319
#title Characterization of Hex2 protein, a negative regulatory element necessary for glucose repression in yeast.
#accession S17254
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submitted to the Protein Sequence Database, July 1996
S67841
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#length 1014 #molecular-weight 112615 #checksum
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91.5%; Score 43; DB 11; Length 1014;
Best Local Similarity 80.0%; Pred. No. 2.88e+01;
Matches 4; Conservative 1; Mismatches 0; Indels (
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##residues 775-1014 ##label PRY
##cross-references EMBL:274324
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##cross-references EMBL:M90540
SNCE S17254
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nonstructural protein, 12.8K - porcine hemagglutinating
encephalomyelitis virus (strain w%72)
#formal_name porcine hemagglutinating encephalomyelitis virus
13.Jan-1996 #sequence_revision 13.Jan-1996 #text_change
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encephalomyelitis virus 13.Jan-1996 #sequence_revision 13.Jan-1996 #text_change
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nonstructural protein NS2 - human coronavirus (strain OC43)
#formal_name human coronavirus
17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
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1-109 ##label VIE
##ccoss-references EMBL:X89863
##ccoss-references #molecular-weight 12818 #checksum 4120
                                            ##cdoss-references EMBL:X89861
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submitted to the EMBL Data Library, July 1995
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#domain fork head DNA-binding domain homology #label FHD #length 228 #molecular-weight 25752 #checksum 8289
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                         Mounir, S.; Talbot, P.J.
Virology (1993) 192:355-360
Human coronavirus OC43 RNA 4 lacks two open reading frames located downstream of the S gene of bovine coronavirus. A44278
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PES-18 protein - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
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##residues 1-264 ##label HO2
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##cross-references EMBL: Z28375
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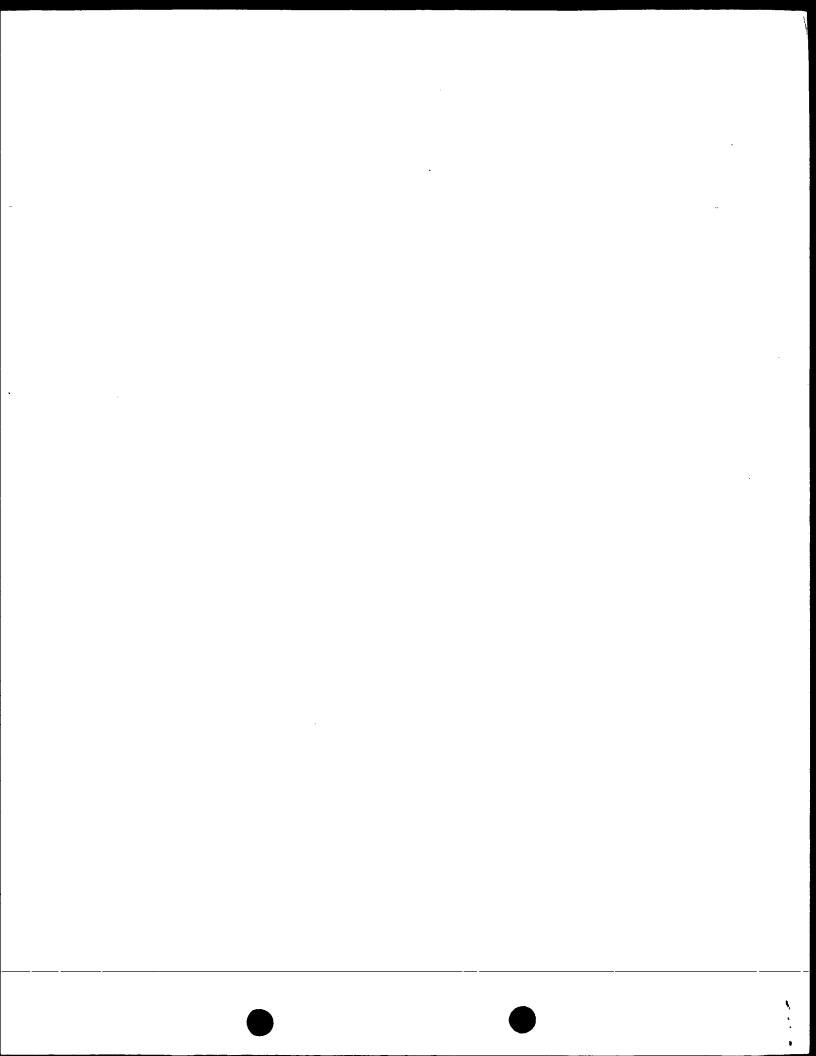
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A47092 #type complete
replication protein repA - Enterococcus faecalis plasmid pAD1
26-May-1994 #sequence_revision 26-May-1994 #text_change
26-May-1994
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                                      #domain fork head DNA-binding domain homology #label FHD #length 264 #molecular-weight 29480 #checksum 3098
                                                                                                                                                                                                                                                                                                                                                                                                                             Weaver, K.E.; Clewell, D.B.; An, F. J. Bacteriol. (1993) 175:1900-1909
Identification, characterization, and nucleotide sequence of a region of Enterococcus faecalis pheromone-responsive plasmid pADI capable of autonomous replication.
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#length 336 #molecular-weight 39031 #checksum 4594
#superfamily fork head DNA-binding domain homology
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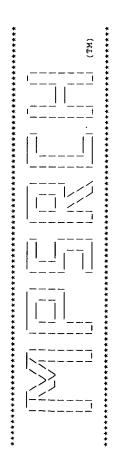
89.4%; Score 42; DB 9; Length 336;
Best Local Similarity 80.0%; Pred. No. 4.41e+01;
Matches 4; Conservative 1; Mismatches 0; Indels
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Search completed: Tue Dec $\ 2\ 14:43:23\ 1997$ Job time : $11\ \text{secs}.$

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:42:45 1997; MasPar time 3.82 Seconds 33.352 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-1 (1-6) from US08915004.pep 47 1 XYHFPK 6 Description: Perfect Score: tle:

PAM 150 Gap 15 Scoring table:

Sequence:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot34
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 20.932; Variance 22.971; scale 0.911 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No	9.76e-01	7.96e+00	7.96e+00	7.96e+00	7.96e+00	7.96e+00	1.32e+01	1.32e+01	2.16e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01	3.51e+01
Description	COLLAGEN ALPHA 1(XVII	6'-AMINOGLYCOSIDE N-A	DIPEPTIDYL PEPTIDASE	DIPEPTIDYL PEPTIDASE	DIPEPTIDYL PEPTIDASE	HEX2 PROTEIN (SRN1 PR	NONSTRUCTURAL PROTEIN	HYPOTHETICAL 40.3 KD	HYPOTHETICAL 29.1 KD	TRAL PROTEIN.	HYPOTHETICAL 23.8 KD	28.1 KD VIRULENCE PRO	28.1 KD VIRULENCE PRO	28.1 KD VIRULENCE PRO		HYPOTHETICAL 32.0 KD	HYPOTHETICAL 34.1 KD	HYPOTHETICAL LYSYL-TR	HYPOTHETICAL LYSYL-TR	PYRUVATE DEHYDROGENAS	HYPOTHETICAL 37.7 KD	MATRIX PROTEIN.
ū	CA1H_MOUSE	AACA_STAAU	DPP6_RAT	DPP6_BOVIN	DPP6_HUMAN	HEX2_YEAST	VNS2_CVHOC	YJY9_YEAST	YCR2_BACTK	TRAL_SALTY	YAL4_SCHPO	VRP1_SALEN	VRP1_SALDU	VRP1_SALCH	COX3_ANOGA	YHWO_YEAST	YLF4_CAEEL	SYK3_HAEIN	SYK3_ECOLI	ODPB_ACHLA	YJEQ_ECOLI	VMAT_SEND5
DB	7	Н	3	m	m	4	10	11	11	σ	11	10	10	10	7	1	11	σ	σ	7	11	10
% Query Match Length	1315	479	859	863	865	1014	109	349	252	101	209	255	255	255	262	283	291	323	325	327		348
% Query Match	100.0	91.5	91.5	91.5	91.5	91.5	89.4	89.4	87.2	85.1	85.1	85.1	85.1	85.1	85.1	85.1	85.1	85.1	85.1	85.1	85.1	85.1
Score	47	43	43	43	43	43	42	42	41	40	40	40	40	40	40	40	40	40	40	40	40	40
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ALIGNMENTS

SIMILARITY). 479 AA; 56855 MW; A8193B91 CRC32;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACETYL-COA BINDING SITE (BY SIMILARITY).
TO OTHERS APHS AND A VPH.
AMINOGLYCOSIDE SUBSTRATES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACA_STAAU STANDARD; PRT; 479 AA.
P14507;
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-OGT-1994 (REL. 30, LAST ANNOTATION UPDATE)
6'-AMINOGLYCOSIDE N-ACETYLTRANSFERASE (EC 2.3.1.-) (AAC(6')) / 2''-AMINOGLYCOSIDE PHOSPHOTRANSFERASE (EC 2.7.1.-) (APH(2'')).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES=E.FAECALIS;
MEDLINE: 86277923.
J. GILMORE K.S., COURVALIN P.;
J. BACTERIOL. 167:631-638(1986).
-!-FUNCTION: RESISTANCE TO GENTAMICIN, TOBRAMYCIN, AND KANAMYCIN.
TOBRAMYCIN AND KANAMYCIN RESISTANCE IS DUE TO THE ACC ACTIVITY, SPECIFIED BY THE FIRST 170 AAA, AND THE GENTAMICIN RESISTANCE IS DUE TO THE APH ACTIVITY ENCODED BY THE CITEMINAL REGION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACETYLTRANSFERASE FROM S.LAVENDULAE. THE C-TERMINAL REGION IS HOMOLOGOUS TO OTHERS APHS, AND TO A VIOMYCIN PHOSPHOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACA-APHD.
STAPHYLOCOCCUS AUREUS, AND ENTEROCOCCUS FAECALIS (STREPTOCOCCUS
                                                                                                                                                                                                                                                                                           TRIPLE-HELICAL REGION 10 (COL10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                      CELL ATTACHMENT SITE (POTENTIAL)
MW; FAE26C53 CRC32;
                                                                                                     NONHELICAL REGION 6 (NC6).
TRIPLE-HELICAL REGION 6 (COL6).
NONHELICAL REGION 7 (NC7).
                     NONHELICAL REGION 4 (NC4).
TRIPLE-HELICAL REGION 4 (COL4).
                                                              NONHELICAL REGION 5 (NC5).
TRIPLE-HELICAL REGION 5 (COL5).
                                                                                                                                                                   (COL7).
                                                                                                                                                                                                                                                  TRIPLE-HELICAL REGION 9 (COL9). NONHELICAL REGION 10 (NC10).
    TRIPLE-HELICAL REGION 3 (COL3).
                                                                                                                                                                                                          TRIPLE-HELICAL REGION 8 (COL8). NONHELICAL REGION 9 (NC9).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1315;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; Length 1315
Pred. No. 9.76e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               NONHELICAL REGION 11 (NC11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M13771; G153586; --
EMBL; M18086; G152948; --
EMBL; M18086; G152948; --
PIR; A256048, 226533; 226533; 226353.
ANTIBIOTIC RESISTANCE; TRANSFERASE; KINASE; ATP-BINDING; ACYLTRANSFERASE; TRANSPOSABLE ELEMENT.
                                                                                                                                                                                      (NC8).
                                                                                                                                                                   TRIPLE-HELICAL REGION 7
NONHELICAL REGION 8 (NC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROUCH D.A., BYRNE M.E., KONG Y.C., SKURRAY R.A., J. GEN. MICROBIOL. 133:3039-3052(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROKARYOTA; FIRMICUTES; COCCI; MICROCOCCACEAE
                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES-S.AUREUS; TRANSPOSON-IN4001;
MEDLINE; 88187650.
                                                                                                                                                                                                                                                                                                                                                                                              134263
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                    982
1000
1315
126
488
894
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408
393
                                                                                                                                                                                                                                                                                                                                                                      892 89
1315 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                           SITE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
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MEDLINE; 9210818.

WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;
PROC. NATL. ACAD. SCI. U.S.A. 89:1942.

PUNCTION: WAD SCI. U.S.A. 89:1942).

- 1 FUNCTION: HAS BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
FUNCTION: HAS NO DIPEPTIDYL AMINOPEPTIDASE ACTIVITY. THE LACK OF
ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTARE RESIDUE
FOR THE SERINE RESIDUE IN THE PROPOSED CAPALYIC TRIAD.

- 1 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).

- 1 TISSUE SPECIFICITY: DEPX-S IS EXPRESSED IN BRAIN AND SOME
PERIPHERAL TISSUES INCLUDING KIDNEY, OVARY, AND TESTIS, IN
CONTRAST DEPX-L IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN
CONTRAST DEPX-L IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN
CONTRAST DEPX-L IS EXPRESSED ALMOST EXCLUSIVELY IN BRAIN
CONTRAST DEPX-L LOUGH AND SIGNER EXPLOSIVELY IN BRAIN
DOMAIN, BUT HAVE LONG AND SIGNET N-TERMINAL EXTRACELLULAR
DOMAIN, BUT HAVE LONG AND SIGNET N-TERMINAL CYTOPHASMIC DOMAINS

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
EMBL: M76426; 6408716; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGPQAQAVAPRERGGAGGRPRFQYQARSDCDEED -> MTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASE; DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
SIGNAL-ANCHOR; ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                      Gaps
                                                                                                                                                                                                                       DPP6_RAT
DPP6_RAT
DPP6_RAT
DPP6_RAT
DP46_101;
01-NOY-1995 (REL. 32, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-REP1996 (REL. 33, LAST ANNOTATION UPDATE)
DIPEPTIDXL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDXL AMINOPEPTIDASE-RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
                                                                   ;
0
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Score 43; DB 1; Length 4/9;
Pred. No. 7.96e+00;
...aarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKEPSASGKSVQQQDQ (IN DPPX-S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 3; Le
Pred. No. 7.96e+00;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B43C0E82 CRC32;
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POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                     Query Match 91.5%;
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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167
168
313
398
398
529
560
807
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                                                                                                              86 yhypk 90
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                                                                                                                                                        2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN
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CARBOHYD
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CARBOHYD
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RC TISSUE-BRAIN;

A MEDINE; 92108018.

RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;

RA WADA K., YOKOTANI N., HUNTER C., DOI K., WENTHOLD R.J., SHIMASAKI S.;

RL PROC. NATL. ACAD. SCI. U.S.A. 98:197-201(1992).

CC -!- FUNCTION. HAX BE INVOLVED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN

CC ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPATATE RESIDUE

FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRAD.

-!- SUBGELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).

-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE BRAIN. DPDX-L.

IS EXPRESSED EXCLUSIVELY IN THE BRAIN WHEREAS DPPX-S IS FOUND IN CC -!- ALTERNATIVE SPLICING. THE SEQUENCE

SHOWN HERE IS THAT OF THE LONG FORM (DPPX-S) AND A LONG FORM (DPPX-L).

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC. SIMILARITY: BELONG TO PEPTIDASE FAMILY.

CC -- SIMILARITY: BELONG TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC. SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).

CC -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC. SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).

CC -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC. SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).

CC -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC. SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).

CC -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC. SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).

CC -- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE PROLIC. SHOWN AS THE PROME. SIGNAL-ANCHOR. ALTERNATIVE SPLICING.

FT TRANSMEM S1GNAL-ANCHOR. ALTERNATIVE SPLICING.

FT TRANSMEM S9 THE PROPERTY.
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PLGAQARAAPRERGGGGAGGRPRPYQARSDCDDED ->
MTAREPNASGRSVQQQEQ (IN DPPX-S).
8DA40472 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                  01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FBF-1996 (REL. 33, LAST ANNOTATION UPDATE)
DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-RELATED PROTEIN) (DIPEPTIDASE VI) (DPPX-L/DPPX-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DIPEPTIDXL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-
RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX-L/DPPX-S).
                                                                                                                                                                                     BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 3; Length 863;
Pred. No. 7.96e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                   863 AA
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               863 AA; 96556 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                   STANDARD;
                                                                                                                                                                                                                                 EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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DPP6_HUMAN
P42658;
01-27
             DPP6_BOVIN
P42659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
CARBOHYD
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CARBOHYD
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RESULT
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RCHGPRAQAAAPREKGGGGGAGGRPRGYQGRSDEED
-> MITAKEPASKGKGYQQGGE (IN DPPX-S).
514C21E2 CRC32;
                MEDLINE; 93372805.

YOKOTANI N. DOI K., WENTHOLD R.J., WADA K.;

HUM. MOL. GEBET. 2:1037-1039(193).

-!-FINCTION: MAY BE INVOLUED IN THE PHYSIOLOGICAL PROCESSES OF BRAIN
FUNCTION: MAY BE DIVED TO THE PHYSIOLOGICAL PROCESSES OF BRAIN
FUNCTION: HAS NO DIPEPTIDEL AMINOPEPTIDASE ACTIVITY. THE LACK OF
ACTIVITY MAY BE DUE TO THE SUBSTITUTION OF AN ASPARTATE RESIDUE
FOR THE SERINE RESIDUE IN THE PROPOSED CATALYTIC TRIAD.
-!- SUBCELLUAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBBLE).
-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN.
-!- ALTERNATIVE PRODUCTS: A SHORT FORM (DPPX-S) AND A LONG FORM
(DPPX-L). ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE
SHOWN HERE IS THAT OF THE LONG FORM (DPPX-L).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9B; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M96859; G306706; -.
EMBL, M96860; G306708; -.
MIM; 126141; -.
HYDROLASE: DIPEPTIDASE; SERINE PROTEASE; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HEX2 PROTEIN (SRN1 PROTEIN).
HEX2 OK SRN1 OR REG1 OR SPP43 OR YDR028C OR YD9813.06C.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-5288C / AB972;
BOWMAN S., BARRELL B., RAJANDREAM M.A.;
SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 3; Le
Pred. No. 7.96e+00;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1014 AA.
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MEDILINE; 91346467.
NIEDERACHER D., ENTIAN K.-D.;
EUR. J. BIOCHEM. 200:311-319(1991).
                                                                                                                                                                                                                                                                                                                                                                            PROLYL OLIGOPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 775-1014 FROM N.A. EIDE L.G., SANDER C., PRYDZ H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 80.0% (les 4; Conservative
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404
471
535
813
813
IISSUE-HIPPOCAMPUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865 AA;
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MEDLINE; 92269840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 yhypk 346
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2 YHFPK 6
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HEX2_YEAST
Q00816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
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CARBOHYD
VARSPLIC
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ID TRAL_SALTY
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                SO OR REPORT SO OS SO OR SERVICE SO OR SERVI
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DK -> EE (IN REF. 1).
N -> K (IN REF. 1).
N -> H (IN REF. 1).
S -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARGMASKÝLHSWKKSDVKPQENGNDSS -> QEVWQASTCT
LGKRVISSHKKMEMTAVRRKNFEVNMKRK
12:1085-1090(1996).
PROCESSING AND NEGATIVE REGULATION OF CLUCOSE REPRESSION. REGULATES THE LEVEL OF TWO ANTIGENS, P43 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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01-FÉB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FÉB-1994 (REL. 28, LAST ANNOTATION UPDATE)
NONSTRUCTURAL PROTEIN NSZ NONSTRUCTURAL 12.9 KD PROTEIN).
HUMAN CORONAVIRUS (STRAIN OC43).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; CORONAVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 4; Length 1014;
Pred. No. 7.96e+00;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 10; Length 109; Pred. No. 1.32e+01; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IN REF. 1).
1014 AA; 112615 MW; 65BA11F7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE: 93297129.
MOUNIE: 93297129.
MOUNIE S., TALLOR.
MOUNIE S., TALLOR.
MOSAGE S., TALLOR.
MOSAGE S., TALLOR.
MOSTRUCTURAL PROTEIN.
SEQUÜNCE 109 AA; 12935 MW; C47B6812 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 109 AA.
                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR.
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Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                   EMBL, M33703; G171666; -.
EMBL, M90540; G172699; -.
EMBL, Z47814; G642300; -.
EMBL, X95966; E225541; -.
PIR; S17254; S17254.
PIR; S32613; S32613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A; SC00434; HEX2
L0001609; REG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 yhypk 342
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YHFPK 6
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2 YHFPK 6
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            YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD;
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ID YJ
AC P4.
DT 01
DT 01
DT 01
            SHELLES
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YCR2_BACTK STANDARD; PRT; 252 AA.

101-MAY-1991 (REL. 18, CREATED)

01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)

01-FEB-1994 (REL. 28, LAST ANNORATION UPDATE)

101-FEB-1994 (REL. 29.1 KD PROTEIN IN CRYB1 S'REGION (ORF2).

BACILLUS THURINGIENSIS (SUBSP. KGRSTAKT).

PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 11; Length 349;
Pred. No. 1.32e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 11; Length 252;
Pred. No. 2.16e+01;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 X 15 AA TANDEM REPEATS.
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
DE HAAN M., SAITS P.H.M., GRIVELL L.A.;
DE HABI M., SAITS P.H.M., ORIVELL L.A.;
DE HABI W., SAITS P.H.M., GRIVELL L.A.;
EMBL; X85972; G758285; --
EMBL; X87611; G854594; --
EMBL; Z49519; G1015655; --
HYPOTHERICAL PROTEIN.
SEQUENCE 349 AA; 40259 MW; C38D06E2 CRC32;
                                                                                                                   HANI J., STUMPF G., DOMDEY H.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2B6BECAB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 (INCOMPLETE).
12 (INCOMPLETE).
13 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIDNER W.R., WHITELEY H.R.;
J. BACTERIOL. 171.965-974(1989).
EMBL, WA3723; G1124821; -.
PIR; B32053; B32053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29110 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 AA;
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=HD-1;
MEDLINE; 89123178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 yqfpk 195
                                                                                               STRAIN-DH484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 yhfpn 8
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STANDARD;
                                                                                                                                                                                                                                                                                         SALMONELLA DUBLIN.
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 PLASMIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 yhfp 138
                                                                                                                                                                     135 yhfp 138
                                                                                                                                                                                      2 YHFP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YHFP 5
                                                                                                                                                                                                                  LT 13
VRP1_SALDU
P24418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRP1_SALCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                    PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-972;
MCLEAN J., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO YEAST SPT10.
EMBL; 267999; G1067220;
-HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 11; Length 209;
Pred. No. 3.51e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                        85.1%; Score 40; DB 9; Length 101; larity 80.0%; Pred. No. 3.51e+01; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
HYPOTHETICAL 23.8 KD PROTEIN C21E11.04 IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                    SPAC21E11.04.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 AA; 23809 MW; DA251012 CRC32;
                                                                                                                                                                               PLASMID; CONJUGATION; OUTER MEMBRANE.
SEQUENCE 101 AA; 12037 MW; 941A2072 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
28.1 KD VIRULENCE PROTEIN.
     01-0CT-1989 (REL. 12, CREATED)
01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                 209 AA
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPVA.
SALMONELLA ENTERITIDIS.
                                                   SALMONELLA TYPHIMURIUM.
PLASMID PED208.
                                                                                                                                                                                                              Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            9 yrfpk 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 yhfp 202
                                  TRAL PROTEIN.
                                                                                                                                                                                                                                                             2 YHFPK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YHFP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 12
VRP1_SALEN
P55219;
                                                                                                                                                                                                                                                                                                 YAL4_SCHPO
Q09927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERTACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEQUENCE FROM N.A.
MEDLINE; 91251759.
KRAUSE M., FOLDES C., FIERER J., HARWOOD J., GUINEY D.;
MOL. MICROBIOL. 5:307-316(1991).
-!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE
STRAIN-ALLI90;
SURDLINE; 9436289F.
SUZUKI S., KOMASE, K., MATSUI H., ABE A., KAWAHARA K., TAMURA Y.,
KUJINA M., DANBARA H., NAKAMURA M., SATO S.;
MICROBIOLOGY 140:1307-1318(1994).
-!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE OF SALMONDELLAS.
-!- SIMILARITY: TO SIMILAR PROTEIN IN OTHER SALMONELLA VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF SALMONELLAS.
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                                                                                                                                                                                                                                                                                         Length 255;
                                                                                                                                                                                                                                                                  Score 40; DB 10; Length 200
Pred. No. 3.51e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 10; Length 255
Pred. No. 3.51e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
28.1 KD VIRULENCE PROTEIN (PROTEIN M3, IN MBA REGION).
8ALMOMELLA CHOLERAE-SUIS (SALMONELLA ENTERICA).
PLASMID PKDSC50.
                                                                                                                                                         EMBL; X56727; G47838; -.
PIR; S15214; S15214.
PLASMID; VIRULENCE.
SEQUENCE 255 AA; 28156 MW; 2455A4CB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-1992 (REL. 21, CREATED)
01-WAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
18-1992 (REL. 21, LAST ANNOTATION UPDATE)
28.1 KD VIRULENCE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 85.1%;
Local Similarity 100.0%;
tes 4; Conservative
                                                                                                                                                                                                                                                                                       Query Match 85.1%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                0; Gaps
                            NUCLETC ACIDS RES. 18:2181-2181(1990).
-!- FUNCTION: NOT KNOWN. THIS PROTEIN IS INVOLVED IN THE VIRULENCE OF SALMONELLAS.
-!- SIMILARITY: TO SIMILAR PROTEIN IN OTHER SALMONELLA VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-63;

BEARD (C.B., HAMM D.M., COLLINS F.H.;

BEARD (C.B., HAMM D.M., COLLINS F.H.;

INSECT MOL. BIOL. 2:103-104 (1993).

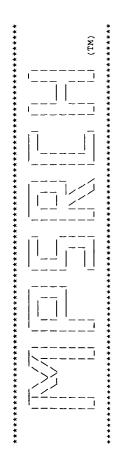
-!- FUNCTION: SUBNNIT I, II, AND III FORM THE FUNCTIONAL CORE OF THE PROXYME COMPLEX.

-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 6 FERRICYTOCHROME C.

EMBL; LO9934; G309062.

CONIDOREDUCTASE; MITOCHONDRION; TRANSMEMBRANE.

SEQUENCE 262 AA; 30132 MW; 73CE1E48 CRC32;
                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 3.51e+01;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tery Match 85.1%; Score 40; DB 2; Length 262; st Local Similarity 80.0%; Pred. No. 3.51e+01; ltches 4; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       P34842;
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANOPHELES GAMBIAE (AFRICAN MALARIA MOSQUITO).
MITOCHONDRION.
EUKARĶOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                             PLASMIDS.
EMBL, X52035; G46897; -.
PIR, S09497; S09497.
SEQUENCE 255 AA; 28184 MW; ECBB81FC CRC32;
                                                                                                                                                                                                                                                                                                                                                             262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: Tue Dec 2 14:42:53 1997 Job time : \mid \theta secs.
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
MEDLINE; 90245675.
MATSUI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 yhfsk 230
                                                                                                                                                                                                                                                       135 yhfp 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHFPK 6
                                                                                                                                                                                                                                                                             RESULT 1'5
ID COX3_ANOGA
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Dec 3 10:06:49 1997; MasPar time 5.21 Seconds 33.068 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-2 (1-14) from US08915004.pep 78 1 XQHSXQEQIFQLXK 14 Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

101610 seqs, 12294212 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq28
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21

Mean 16.442; Variance 48.941; scale 0.336 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

d. No.	43e-02	43e-02	43e-02	43e-02	43e-02	3e-02	43e-02	43e-02	43e-02	43e-02	43e-02	43e-02	3e-02	43e-02	3e-02	3e-02	3e-02	3e-02	3e-05	19e+02
Pred.	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	
Description	Osteoclastogenesis in	Mutated OCIF, OCIF-CD	Mutated OCIF, OCIF-CS	Mutated OCIF, OCIF-DD	Mutated OCIF, OCIF-CC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mature osteoclastogen	Human tumour necrosis	Mutated OCIF, OCIF-CB	Mutated OCIF, OCIF-CL	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C1	Full length osteoclas	Prostate-specific mem
QI	R99922	R99944	R99949	R99941	R99943	R99939	R99937	R99938	R99936	R99924	R99357	R99948	R99942	R99934	R99932	R99935	R99933	R99931	R99925	W02241
DB	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20		~	20	20	18
Length	14	272	321	327	351	359	359	360	360	380	390	393	399	401	401	401	401	401	401	22
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	59.0
Score	78	78	78	78	78	78	78	78	78	78	7.8	7.8	78	78	78	78	78	78	78	46
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R55102	R72367	R72368	1	φ	1	ᅼ	7	?	3	9	3	2	ō	~	7	9	8	0	22	7	2	2	5	2	ALIGNMENTS	, ,		ory factor p
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4		3	4	5	6	7	8	9	0	1 4	2	3 4	4 4	5 4	6 4	7	8	9	0	1 4	2 4	3 4	4 4	5 4		H C C C C C C		22-APR-1997 Osteoclasto
0	7	7	7	7	7	7	7	7	m	m	m	e	m	m	m	m	m	æ	4	4	4	4	4	4		SUI		OE OE

1 standard; peptide; 14 AA. 2.	73-787. 22-APR-1997 (first entry) Osteoclastogenesis inhibitory factor peptide fragment #2. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;	•	Location/Qualifiers	<pre>fisc_difference 1 foote= "Any amino acid"</pre>	difference 5	note= "Any amino acid" Aisc difference 13	"Any amino acid"	6217-A1.				JP-207508.	SNOW BRAND MILK PROD CO LTD.	Higashio K, Kobayashi E, Mochizuki S,	jawa N, Shima N, Isuda E, Ueda M, Yaho K, Yasuda H; 96-402320/40.	DNA encoding osteoclastogenesis inhibitory factor protein - useful	one resorption control, esp. treatment of osteoporosis	Page 61; 183pp; Japanese.	Sequences given in R99921-23 and R9992b represent iragments or	the OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing	conditions and 120 kD under non-reducing conditions. The protein is			lost after 10 Mins at 90 meg.c. Other is useful in the control of bone resorption and therefore in the treatment and prevention of	of bone resorption, e.g. osteoporosis.
RESULT 1 ID R99922 standard AC R99922.	22-APR-1997 (first Osteoclastogenesis Osteoclastogenesis	osteoporosis. Homo sapiens.	Key	Misc_difference /note= "Any amin	Misc_difference 5	/note= "Any amino Misc difference 13	/note= "Any ami	W09626217-A1.					SNOW	Goto M, Higash	Nakagawa N, Shi WPI; 96-402320/	ncod	for bone resorp	Claim 1; Page 6	The sequences g	The OCIF has a	conditions and	adsorbed onto c	lowered after 1	bone resorption	disorders of bo
RES	SEE	N S	E	FT	Ë	F F	FT	ЬN	PD	ΡF	PR	PR	PA	7 6	P.I.	БŢ	ΡŢ	D D		ט נ	S	ပ္ပ	ဥ	38	8

Score 78; DB 20; Length 14; Pred. No. 2.43e-02; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative

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243 ghssqeqtfqllk 255
        N-PSDB; T33179.
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N-PSDB, T3317
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                                                                                                                                                                                       Mutated OCIF, OCIF-CDD2.
Ostebclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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Yasuda H;
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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20-FBB-1996; JO0374.
20-FBB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCOM, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSpB; Ţ33174.
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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R99944 standard; Protein; 272 AA.
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Best Local Similarity 84.68;
Matches 11; Conservative
                                                                                                                                                                   (first entry)
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/note= "Mature OCIF-CDD2"
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/note= "Mature OCIF-CSph"
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/note= "Signal peptide"
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  OHSXQEQTFOLXK 14
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 253-326 of the mature OCIF protein are deleted. The OCIF of the invention on and 120 Kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C or 10 mins at 20 deg.C. OCIF is useful in the control of bone resorption and therefore
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23-APR-1997 (first entry)
Mutated OCIF, OCIF-DDD2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 78; DB 20; Length 321; Best Local Similarity 84.6%; Pred. No. 2.43e-02; Matches 11; Conservative 0; Mismatches 2; Indels
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JÜL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Robayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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Misc_difference 273..274
Misc_difference 273..274
WO9626217_A1.
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Best Local Similarity 84.6%;
Matches 11; Conservative
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/note= "Mature OCIF-DDD2"
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Goto M, Higashio K,
Nakagawa N, Shima N,
WPI; 96-402320/40.
N-PSDB; T33169.
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                                                                                                                                                                                                                                                                                              DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 65; Page 119-121, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CC in which amino acids 331-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C. and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutated OCIF, OCIF-DCR4. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                        Morinaga T;
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Pred. No. 2.43e-02;
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20-FEB-1995; JP-054977.
21-UTL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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/note= "Positition of deletion, delta 123-164"
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
SNOW BRAND MILK PROD CO LTD.
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R99939 standard; Protein; 359 AA.
                                          II 5
R99943 standard; Protein; 351 AA.
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84.6%;
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/note= "Mature OCIF-DCR4"
                                                                                                                                         Peptide 1.21
/note= "Signal peptide"
Protein 22.351
/note= "Mature OCIF-CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 ghssgegtfgllk 255
                                                                                     Mutated OCIF, OCIF-CC.
2 QHSXQEQTFQLXK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 AA;
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                                                                                                           osteoporosis.
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                                                                                                                      Synthetic.
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for bone resorption control, esp. treatment of osteporosis

Claim 47; Page 107-109; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR2 in which amino acids 43-84 of the mature OCIF protein are deleted. The OCIF of the invention and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. and 05-C. and 05-
                                                                                                                                                                                                                                                                                                                                                                   osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR4 in which amino acids 123-164 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C. and is lost after 10 mins at 70 deg.C. ocif is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                    DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 53; Page 111-113; 183pp; Japanese.
This sequence represents a mutated version of the full length
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Yasuda H;
                                                     Yasuda H;
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b, 2,43e-02;
2; Indels
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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20-FEB-1996; JO0374.
20-FEB-1995; JP-05497.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; T33167.
Kobayashi F, Mochizuki S,
Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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/note= "Position of deletion, delta 43-84"
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Pred. No. 2
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84.6%;
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Best Local Similarity 84.6%;
Matches 11; Conservative
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/note= "Mature OCIF-DCR2"
Misc_difference 63..64
/note= "party
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Best Local Similarity 84.6%;
Matches 11; Conservative
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"Signal peptide"
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.c. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-DCR3.
Osteopolastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morinaga T;
Yasuda H;
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI:|96-402320/40.
N-PSpB; T33168
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/note= "Position of deletion, delta 85-122"
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Protein 22.360
/note= "Marure OCIF-DCRI"
Misclafiference 22.23
/note= "Position of deletion, delta 2-42"
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
SKNW) SNOW BRAND MILK PROD CO LTD.
GOCO |M, Higashio K, Kobayashi F, M
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R99938 standard; Protein; 360 AA.
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Local Similarity 84.6%;
les 11; Conservative
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"Signal peptide"
                       201 qhssqeqtfqllk 213
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                                                                                        2 OHSXQEQIFQLXK 14
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29-AUG-1996.
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for bone resorption control, esp. treatment of osteoporosis.

Claim 44: Page 105-107; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents oCIF-DCRI in which amino acids 2-42 of the area of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCRI in which amino acids 2-42 of the macure OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto action-exchangers or hepzin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the example of the control of bone resorption and therefore in the example of the control of bone resorption, e.g.
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Mature osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In the encoding osteoclastogenesis inhibitory factor, protein - useful for bone resorption control, esp. treatment of osteoporosis claim 6; Page 62-64; 183pp; Japanese.

This sequence represents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 10 mins at 56 deg.C., and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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29-A0G-1996.
20-REB-1996.
20-FEB-1995. JP-054977.
21-JUL-1995. JP-207508.
21-JUL-1995. JP-207508.
GOLO M, H19ashio K, Kobayashi F, Mochizuki S, Morinaga T: Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; N-PSDB; T36685.
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Yasuda H;
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78; DB 20; Length 380
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
20-FEB-1996; J00374.
R 20-FEB-1995; JP-054977.
R 21-JUL-1995; JP-207508.
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
PA (SNOW ) F. M. Higashio K, Kobayashi F, Mochizuki S, Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R99924 standard; Protein; 380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 ghssgegtfgllk 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 qhssqeqtfqllk 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Claim 80; Page 126-128; 183pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                       RESULT
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 ô
                                                                                                                                                                                                                                                              New human turnour necrosis factor receptor - used to develop prods.

T for treating e.g. tumnurs, infection, auto:immune disease, graft rejection cytotoxicity or inflammation.

Claim 14: Fig. 15pp: English.

Claim 14: Fig. 15pp: English.

C The receptor binds to TNF, and in particular, TNF-beta.

The receptor may be used for screening for antagonists and agonists of the receptor and for ligands for the receptor. Such agonists of the receptor and for ligands for the receptor. Such agonists may differentiation, to mediate the immune response and anti-viral response, to requiate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat untoimmune diseases, inflammation, septic shock, to inhibit graft.

Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1997 (first entry)
Mutated OCIF, OCIF-CBst.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                        Human tumour necrosis factor receptor.
Tumour necrosis facor; TNF; receptor; TNF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW JOWN BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78; DB 20; Dred. No. 2.43e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                              septic shock; graft-versus-host; apoptosis.
                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R99948 standard; Protein; 393 AA.
                      R99357 standard; Protein; 390 AA.
                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                          Fleischmann RD, Greene JM; WPI; 96-433821/43.
N-PSDB; T35475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%;
Local Similarity 84.6%;
                                              05-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein 22.393 /note= "Mature OCIF-CBst"
                                                                                                                                                                  19-SEP-1996.
15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 ghssgegtfgllk 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 OHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1996.
20-FEB-1996; J00374.
                                                                                                                                            /label= sig_peptide
WO9628546-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc_difference 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Gln371Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T33178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9626217-A1.
                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                   R99357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
          RESULT
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                        osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CBst in which Gln 371 is substituted by sequence represents OCIF-CBst in which Gln 371 is substituted by the and and maino acids 373-380 of the mature OCIF protein are deleted. These changes are caused by the introduction of a restriction site in the bwa encoding this protein. The OCIF of the invention has a molecular weight by SD-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C. and Mins at 56 deg. C. and is lost after 10 mins at 70 deg. C. ocif is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
This sequence represents a mutated version of the full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78; DB 20; Length 399; Pred. No. 2.43e-02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 78; DB 20; Length 393;
Pred. No. 2.43e-02;
'''...a+rhes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 13
R99942 standard; Protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
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/note= "Signal peptide"
Protein 22..399
/note= "Mature OCIF-CL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 qhssqeqtfqllk 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 ghssgegtfgllk 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 OHSXOEOTFOLXK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-1996.
20-FEB-1996; J00374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9626217-A1.
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243 qhssqeqtfqllk 255
                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                            Dp
  ò
                                                                                                                                                                                                                                                                                    DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 38; Page 100-102; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22S in which the 27nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C ocif is useful in the control of bone resorption and therefore in the control of bone resorption and therefore the control of bone resorption and therefore the control of the control of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                               22-Apr-1997 (first entry)
Mutated OCIF, OCIF-C22S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                             Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB 20; Length 401;
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
                                                                                                                                                                               29-4021996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLD M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; Ţ33164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09626217-A1.
29-AUG-1996.
20-FBB-1995. JD-054977.
21-UUL-1995; JP-054977.
21-UUL-1995; JP-207508.
6SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCON H Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
T |14
R99934 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7. 15
R99932 standard; Protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide 1..21
/note= "Signal peptide"
Protein 22..401
/note= "Mature 02F-C205"
Misc_difference 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.6%;
Best Local II; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1997 (first entry)
                                                                                                                          Protein 22.401
/note= "Mature OCIF-C228"
                                                                                                   Peptide 1..21
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutated OCIF, OCIF-C20S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 qhssqeqtfqllk 255
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                                                                                                                                       /note= "Mature OCIF
Misc_difference 277
                                                                                                                                                            /label= C22S
W09626217-A1.
                                                                    osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis
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                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 41, Page 103-105, 183pp; Japanses.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C23S in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Yasuda H;
                         DNA encoding osteoclastogenesis inhibitory factor protein for bone resorption control, esp. treatment of osteoporosis claim 32; Page 96-98; 183pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78; DB 20; Length 401;
Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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Pred. No. 2.43e-02;
0; Mismatches 2; Indels
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20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
SNOW BRAND MILK PROD CO LTD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
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R99935 standard; Protein; 401 AA.
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84.6%;
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22-APR-1997 (first_entry)
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Best Local Similarity 84.6%;
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/note= "Mature OCIF-C23S"
Misc_difference 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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N-PSDB; T33162
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                                                                                                                                                                                                                                                                                                                                                                                                                             osteoporosis
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Matches
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21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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                                                                                                                           22-APR-1997 (first entry)
Mutated OCIF, OCIF-C21S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AFR-1997 (first entry)
Mutated OCIF, OCIF-C19S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0; Mismatches 2; Indels
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21-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
5NOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; Ţ33163.
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                                                                               T 17
R99933 standard; Protein; 401 AA.
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Local Similarity 84.6%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                         Protein 22..401
/note= "Mature OCIF-C215"
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Misc_difference 195
                                                                                                                                                                                                                                                                     Peptide 1..21
/note= "Signal peptide"
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/note= "Signal peptide" / 401
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
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2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                   Misc_difference 277
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W09626217-A1.
                                                                                                                                                                                                                                                                                                                                                                        /label= C21S
W09626217-A1.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 29; Page 94-96; 183pp; Japanese.
This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C19S in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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            Morinaga T;
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Yasuda H;
                                    Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 401;
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Pred. No. 2.43e-02;
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Pred. No. 2.43e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
   F, Mochizuki S,
Ueda M, Yano K,
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F,
Makagawa N, Shima N, Tsuda E, Ued
WPI; 96-40232/40.
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/note= "Mature OCIF, claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 84.6%;
Matches 11; Conservative
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/note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                          DNA encoding alternatively spliced prostate-specific membrane antigen - useful to develop prods. for detecting haematogenous micrometastic tumour cells, or prostate cancer progression Example 1; Page 49; 284pp; English.

Tryptic peptides (W02237-45) were obtd. from the human prostate-specific membrane (PSM) antigen (see also W0224) and used to design primers (T36795-808) utilised in the isolation of a CDNA clone (T36785) coding for PSM; primers I-L (T36801-04) are based on amino acids 14-19 of peptide 2T4 (W02241). The isolated CDNA and PSM protein are useful in developing methods for the diagnosis and treatment of prostate cancer and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate-specific membrane antigen peptide fragment.

Prostate-specific membrane antigen; PSM, prostate cancer;
transmembrane glycoprotein; imaging; targeting; tumour detection;
antibody detection; sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fair WR, Heston WDW, Israeli RS;
WPI: 94-167129/20.
Prostate-specific membrane antigen and DNA encoding it - is useful for detecting haematogenous micro-metastatic tumour cells and for identifying ligands which bind to PSM Ag Example; Page 46; 196pp; English
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                                                                                            Prostate-specific membrane antigen peptide 2T34 6.
Prostate-specific membrane antigen; PSM; prostate cancer;
metaștasis; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.0%; Score 46; DB 18; Length 22; Best Local Similarity 75.0%; Pred. No. 1.19e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                           (SLOK ) SLOAN KETTERING INST CANCER RES.
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                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                         Heston WDW, Israeli RS;
                                                                                                                                                                /note = "unidentified amino acid"
Misc_difference 5
/note = "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 21
R55102 standard; Peptide; 22 AA.
                                                          W02241 standard; Peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc difference 3
/note= "unidentified residue"
Misc difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "unidentified residue" WO9409820-A.
                                                                                  (first entry)
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                                                                                                                                                                                                                29-AŭG-1996.
23-FEB-1996: U02424.
24-FEB-1995: US-394152.
02-JÜN-1995: US-470735.
02-JÜN-1995: US-466381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MÀY-1994.
05-NOV-1993; U10624.
05-NOV-1992; US-973337.
96-402365/40.
                                                                                                                                                        Misc_difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eqnfqlak 22
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                                                                                                                                                                                                  WO9626272-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo|sapiens.
                                                                                                                                   Homo|sapiens.
                                                                                  05-NÓV-1996
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Pralutation of safety of a chemical cpd. - using recombinant yeast

Pralutation of safety of a chemical cpd. - using recombinant yeast

Pralutation of safety of a chemical cpd. - using recombinant yeast

Examines; Page 49-51; 124pp; English.

Pramine acid sequence of the human auxillary cytochrome P450 species

Crafe. The cDNA was amplified by PCR using the primers 0877514. The

product was cloned into the yeast expression vectors pAAHSN or pARRR to

crafe product the vectors p2A6 for the expression of the cytochrome P450 alone

or p2A6R for co-expression with the yeast NADPH-P450 reductase.

Crompound by reacting the chemical compound with recombinantly produced

compound by reacting the chemical compound with recombinantly produced

compound by reacting the chemical compound with recombinantly produced

compound by an exist NADPH-P450 reductase, either as a fused protein or

(087718-32), and yeast NADPH-P450 reductase, either as a fused protein or

in cellextracts, and analysing the resulting metabolite to assess the

safety of the chemical compound, or its metabolite, will be converted into

a carcinogenic or mutagenic form through metabolism in the liver.
The inventors attempted to sequence the PSM Ag by modified Edman degradation. Peptides (R55098-107) that gave clear dominant peaks on HPLC from the digested PSM Ag sample were used. Some of the residues were unidentified, and others were present at very low levels and identified with lower confidence. Some of these peptides were used to design primers to carry out PCR to identify cDNA clones were used to design primers to carry out PCR to identify cDNA clones cancoding the PSM Ag. R55102 was used to design primers 65527-30.

A clone, IN-20 was identified as a partial PSM sequence.

The full PSM Ag sequence is shown in R55097 and is encoded by 065520. The PSM coding sequence is useful for suppressing or modulating the metastatic ability of prostate tumour cells to grow, or for eliminating them. The protein is useful to identify or purify ligands of the Ag. It is also an attractive target for Ab-directed in imaging and targeting of prostatic tumour deposits.
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Human cytochrome P450; amplification; PCR; primer; expression vector; yeast NADPH-P450 reductase; safety; fusion protein; metabolite; carcinogen; mutagen; liver metabolism.

Homo sapiens.
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0; Mismatches 2; Indels
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Pred. No. 1.19e+02;
3; Mismatches 1;
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20-JUL-1994; 111298.
20-JUL-1993; JP-201120.
21-JUL-1993; JP-208246.
30-JUL-1993; JP-208279.
(HAYA/) HAYASHI K.
(SUMC) SUMITOWO CHEM CO LID.
HAYASHI K, RANGKO H, KOMAI K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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Local Similarity
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N-PSDB; T28387
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J08027195-A.
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                                                                                                                                                                                                                                                                                                                                                For a variant of safety of a chemical cpd. - using recombinant yeast expressing human cytochrome p450 and a yeast NADPH-P450 reductase Examples; page 53-55, 124pp; English.

Examples; page 53-55, 124pp; English.

The amino acid sequence of the human auxillary cytochrome P450 species 2A6 variant 1. This variant contains a variation at residue 476. And to Lys, caused by a variation at base 1427. G to A in the DNA sequence. The CDNA was amplified by PCR using the primers (87751-4. The product was cloned into the yeast expression vectors pAAH5N or pAHRR to produce the vectors p2A6 variant 1 for the expression of the cytochrome P450 alone or p2A6R variant 1 for the expression with the yeast NADPH-P450 reductase. The vectors are used in a method for evaluating the safety of a chemical compound by reacting the chemical compound with recombinantly produced human cytochrome P450 molecular species 1A2 (087714), 2C9 (087715), 2E1 (087716), or 3A4 (087718), or their auxillary species and variants of cellextracts, and analysing the resulting metabolite to assess the safety of the chemical compound, or its metabolite, will be converted into a carcinogenic or mutagenic form through metabolism in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-0cr-1996 (first entry)

Muman cytochrome P450 molecular species 2A6 variant #1 protein.

Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;

Human cytochrome p450; amplified; PCR; polymerase chain reaction; primer;

Liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;

evaluation; safety; fusion protein; metabolite; detoxification;
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                                                                Human auxillary cytochrome P450 species 2A6 variant 1 protein. Human cytochrome P450; amplification; PCR; primer; expression vector; yeast NADPH-P450 reductaes; safety; fusion protein; metabolite; carcinogen; mutagen; liver metabolism.
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Pred. No. 1.19e+02;
...matches 1; Indels 0;
                                                                                                                                                                                                                                                                                             Kaneko H, Komai K, Nakatsuka I, Sakaki T;
                                                                                                                                       Location/Qualifiers
                    R72368 standard; Protein; 494 AA.
R72368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R93174 standard; Protein; 494 AA.
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20-JUL-1993; JP-201120.
30-JUL-1993; JP-208279.
17-JUN-1994; JP-136053.
(SUMO ) SUMITOMO CHEM CO LID.
WPI; 96-182311/19.
                                                                                                                                                                                                                                                              (HAYA/) HAYASHI K.
(SUMO) SUMITOMO CHEM CO LTD.
Hayashi K, Kaneko H, Komai I
                                                                                                                                                                /note= "Arg to Lys variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.0%;
Similarity 55.6%;
5; Conservative
                                                 14-NOV-1995 (first entry)
                                                                                                                                                                                                         20-JUL-1994; 111298.
20-JUL-1993; JP-201120.
21-JUL-1993; JP-180246.
30-JUL-1993; JP-208279.
                                                                                                                                                   Misc_difference 476
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Best Local Similarity
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                                                                                                                        Homo sapiens.
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J08056695-A.
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                                                                                                                                                                           EP-644267-A.
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                                                                                                                                                                                             22-MAR-1995
                                                                                                                                                                                                                                                                                                              Yabusaki
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        RESULT
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Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NaDPH reductase to determine whether PT human cytochrome P450 and yeast NaDPH reductase to determine whether PT the analyte cpd. is detoxified or metabolised to a carcinogen Example 1; Page 33-35; 74pp; Japanese CC This is the amino acid sequence of the human cytochrome P450 molecular cospecies 2A6 variant #1 protein. The corresp, gene was amplified from a human liver derived cDNA library as 2 fragments of 0.6 and 0.9 kb using primers 126941-44. The prod. was cloned into the yeast expression vector primers 126941-44. The prod. was cloned into the yeast expression vector copadisk to generate plasmid p2A6 for prodn. of the cytochrome only or into the vector paner to generate the plasmid p2A6R for co-prodn. with the cyeast NADPH-P450 reductase. The sequence is placed under control of the cyeast Abh gene promoter and terminator.

CT he vectors are used in a method for evaluating the safety of a cpd. by creacting the test cpd. with recombinantly produced human cytochrome P450 conting the test cpd. with recombinantly produced human cytochrome P450 conting the test cpd. with recombinantly produced human cytochrome P450 conting the test cpd. with recombinantly produced human cytochrome P450 conting the test cpd. with recombinantly produced human cytochrome P450 conting the as a fused protein or as a coll extract) and analysing the central rendered carcinogenic or "unsafe" if it is not detoxified or is metabolised to a carcinogenic cpd. "is considered "safe" if it is not detoxified or is Sequence 494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Human derived cytochrome, P4502A6.
Human derived cytochrome, P4502A6; commercial cDNA library; yeast;
transfection; recombinant production; expression vector; mammal;
immunisation; sensitisation; antibody; determination; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody recognising human derived cytochrome P4502A6 - allows specific detection of cytochrome P450 species in humans S Example 1. Pages 11-13; 13pp; Japenese.

The present sequence is the human derived cytochrome (HDC) P4502A6, which was obtd. from a commercial cDNA library. Yeast C were transfected with an expression vector confg. the HDC cDNA, cultured and then disrupted to give a microsomal fraction. The HDC was purified from the fraction, and used to immunise and ansientiese a mammal. Blood was drawn from the mammal, and an anti-HDC antibody isolated The antibody obtd. recognises HDC P4502A6, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC P450 spp..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 1.19e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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R81466;
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13-JUL-1994; JP-161550,
(SUMO ) SUMMITIONO CHEM CO LID.
WPPI; 96-136336/14.
N-PSDB; T17409.
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55.6%;
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Best Local Similarity 55.6%;
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DE R9315 standard; Protein; 494 AA.

AC 19315: Standard; Protein; 494 AA.

BE HUNGYT-1996 (first entry)

E HUNGYT-1996 (first entry)

E HUNGH CYCCHOME P450; amplified; PCR; polymerase chain reaction; primer;

KW HUNG CYCCHOME P450; amplified; PCR; polymerase chain reaction; primer;

KW ACTAL1995 (PASE); expression vector; NADPR-P450 reductase; AbH gene promoter;

KW CATCHOMERS (PASE)

BY 100-MR-1996

BY 10-MR-1995

BY 10-M
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Query Match
Best Local Similarity 55.6%; Pred. No. 1.19e+02;
Matches 5; Conservative 3; Mismatches 1; Indels
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0; Gaps

Search completed: Wed Dec 3 10:06:57 1997 Job time 8 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:44:39 1997; MasPar time 2.99 Seconds 135.144 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-2 (1-14) from US08915004.pep 78 1 XQHSXQEQTFQLXK 14 Itle: Description: Perfect Score:

Sequence:

91006 seqs, 28888923 residues Searched:

PAM 150 Gap 15

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir51
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 22.756; Variance 33.196; scale 0.686 Statistics:

SUMMARIES

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Description	gene H4(D10S170) pro	El protein - human p	El protein - human p	eye development prot	nuclear receptor pro	DR-78 protein - frui	ecdysone-inducible p	involucrin - ring-ta	El protein - human p	phospholipase A2 rec	tyrocidine synthetas	methylgalactoside pe	T-cell receptor delt	involucrin - western	involucrin - mouse	El protein - human p	amine oxidase (flavi	amine oxidase (flavi	exoP protein - Rhizo	probable succinoglyc	hypothetical protein
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Primer-directed sequencing of human papillomavirus types.
S36546
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El protein - human papillomavirus type 26
#formal_name human papillomavirus type 26
20.Feb-1995 #sequence_revision 20.Feb-1995 #text_change
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melanogaster)
                                                                             #Superfamily papillomavirus El protein early protein #length 634 #molecular-weight 71684 #checksum 6865
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Best Local Similarity 54.5%; Pred. No. 3.38e+00;
Matches 6; Conservative 3; Mismatches 2; Indels
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CLASSIFICATION #superfamily papillomavirus El protein
                translation not shown
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Blochim. Biophys. Acta (1993) 1216:339-341
Brochim. novel Drosophila melanogaster genomic DNA fragment highly homologous to the DNA-binding domain of thyroid hormone-retinoic acid-vitamin D receptor subfamily.
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#formal_name Drosophila melanogaster
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DR-78 protein - fruit fly (Drosophila melanogaster)
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larity 54.5%; Pred. No. 5.14e+00;
Conservative 3; Mismatches 2; Indels
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Pred. No. 5.14e+00;
3; Mismatches 2; Indels
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The terminal differentiation of keratinocytes, this protein
If During the terminal differentiation of keratinocytes, this protein
from the cytosol becomes cross-linked to membrane proteins by
transglutaminase and incorporated into an insoluble, cross-linked
envelope under the plasma membrane.
envelope under the plasma membrane.
FICATION #superfamily involuciin
DS cornified cell envelope, duplication; epidermis; tandem
                                                                                                     Stone, B.L.; Thummel, C.S.
Cell (1993) 75:307-320
The Drosophila 78C early late puff contains E78, an
ecdysone-inducible gene that encodes a novel member of the
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Cell (1988) 54:491-496
Remodeling of the involucrin gene during primate evolution.
A43733
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#formal_name human papillomavirus type 30
20.Feb-1995 #sequence_revision 20-Feb-1995 #text_change
336505
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           involucrin - ring-tailed lemur
#formal_name Lemur catta #common_name ring-tailed lemur
20.Feb-1993 #sequence_revision 23-Feb-1996 #text_change
                #formal_name Drosophila melanogaster
03-May-1994_#sequence_revision 03-May-1994 #text_change
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                                                                                                                                                                                                                                                                             alternative splicing
#length 864 #molecular-weight 95792 #checksum 3050
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#length 450 #molecular-weight 50445 #checksum 4455
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                                                                                                                                                                                                                                                                                                                                 Length 864;
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Pred. No. 5.14e+00;
...matches 2; Indels
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Pred. No. 7.78e+00;
4; Mismatches 3; Indels
                                                                                                                                                                       nuclear hormone receptor superfamily.
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##cross-references GB:U01087
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atches 6; Consormations
   melanogaster)
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Best Local Similarity 46.2%;
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A43733
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#domain fibronectin type II repeat homology #label 2FI\
#domain C-type lectin homology #label LCH
#length 1458 #molecular-weight 167199 #checksum 6528
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J. Bacteriol. (1989) 171:4881-4887
Gene cluster containing the genes for tyrocidine synthetases
I and 2 from Bacillus brevis: evidence for an operon.
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J. Biol. Chem. (1994) 269:1575-1578
Cloning and expression of a membrane receptor for secretory
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submitted to the EMBL Data Library, August 1993
Primer-directed sequencing of human papillomavirus types.
836505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A49707 #type complete
phospholipase A2 receptor precursor - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
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09-Sep-1995
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23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change
                                                                                          ##molecule_type DNA
##residues
##residues 1-631 ##label DEL
##cross-references EMBL:X74474
CLASSIFICATION #superfamily papillomavirus El protein
KEYWORDS #superfamily protein
#length 631 #molecular-weight 71809 #checksum 8022
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CLASSIFICATION #superfamily phos
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#accession B33956
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Local Similarity 53.8%;
nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                           methylgalactoside permease ATP-binding protein (mglA) homolog - Haemophilus influenzae (strain Rd KW20) #formal_name Haemophilus influenzae 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kirkness, B.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.; Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.; FitzBugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton, M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geogragen, N.S.M.; Gnehm, C.L.; McDonald, L.A.; Science (1995) 269:496-512
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  *superfamily alpha-aminoadipyl-cysteinyl-valine synthetase; acetate--CoA ligase homology; acyl carrier protein homology; gramicidin S synthetase I repeat homology
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EMBO J. (1993) 12:715-724
Divergent evolution of T cell repertoires: extensive
diversity and developmentally regulated expression of the
sheep gamma-delta T cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
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##nocle named as homolog to a protein from Escherichia coli
CLASSIFICATION #superfamily malk protein homology
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#formal_name Ovis orientalis aries, Ovis ammon aries
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03 Feb-1994 #sequence_revision 03-Feb-1994 #text_change
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#domain malk protein homology #label MK2
th 506 #molecular-weight 56567 #checksum 3128
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                                                                                                                         Length 245;
                                                                                                                                                               1; Indels
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                                                                                                                       Score 49; DB 6; LA Pred. No. 1.75e+01;
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3; Mismatches 4
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                                                                               #length 245 #checksum 6032
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##residue
                                                                                                                       Query Match
Best Local Similarity 66.7%;
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Best Local Similarity 46.2%;
Matches 6; Conservative
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CLASSIFICATION
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Djian, P.; Green, H. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:5321-5325 Involucrin gene of tarsioids and other primates: alternatives in evolution of the segment of repeats. A43704
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TION *superfamily involucrin cornified cell envelope; duplication; epidermis; tandem
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##residues 1-467 ##label RES
##cross-references GB:L28819; NID:9454419
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The involucrin genes of the mouse and the rat: study of their
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#formal_name Tarsius bancanus #common_name western tarsier
20-Feb-1993 #sequence_revision 23-Feb-1996 #text_change
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                                                                                                                                                                                                                                                         DB 14; Length 139;
                                                                                                                                                                                                                               Score 48; DB 14; Leuyller Pred. No. 2.61e+01;
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3; Mismatches 4; Indels
preliminary; translation not shown
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                                                                      ##residues 1-139 ##label HEI
##cross-references EMBL:212997
# #length 139 #checksum 4472
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Local Similarity 46.2%;
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                                   ##molecule_type mRNA
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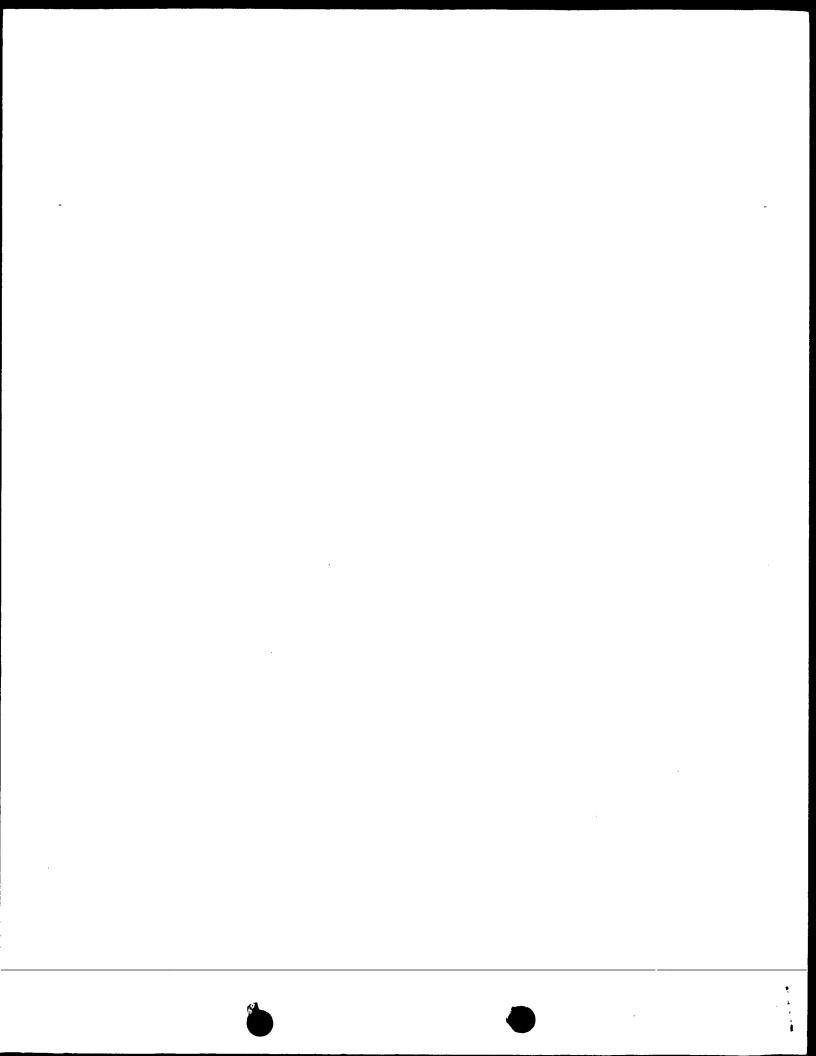
CLASSIFICATION #superfamily involuctin
KEYWORDS cornified cell envelope; duplication; epidermis; tandem
repeat repeat #length 467 #molecular-weight 54919 #checksum 5202

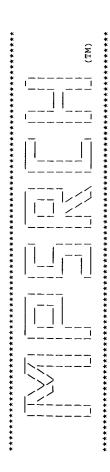
Query Match 61.5%; Score 48; DB 3; Length 467; Best Local Similarity 46.2%; Pred. No. 2.61e+01; Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

92 gqelqeqelhlek 104 |: ||| ::| | 2 QHSXQEQTFQLXK 14 ΩQ

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Search completed: Tue Dec 2 14:44:51 1997 Job time: 12 secs.





Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:44:12 1997; MasPar time 2.03 Seconds 145.979 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-2 (1-14) from US08915004.pep 78 1 XQHSXQEQTFQLXK 14 Description: Perfect Score: tle:

Sequence:

PAM 150 Gap 15 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 23.758; Variance 28.025; scale 0.848 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No	7.11e-01	/.lle-Ul	1.91e+00	1.91e+00	3.09e+00	4.97e+00	7.94e+00	7.94e+00	7.94e+00	7.94e+00	7.94e+00	7.94e+00	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.26e+01	1.98e+01	1.98e+01	1.98e+01
Description	PROTEIN	REPLICATION PROTEIN E		REPLICATION PROTEIN E	180 KD SECRETORY PHOS	GALACTOSIDE TRANSPORT	INVOLUCRIN.	INVOLUCRIN.	REPLICATION PROTEIN E	AMINE OXIDASE PRECURS	COPPER AMINE OXIDASE	SUCCINOGLYCAN BIOSYNT	ANTHRANILATE PHOSPHOR	CAMP-DEPENDENT PROTEI	TRANSCRIPTIONAL ENHAN	TRANSCRIPTIONAL ENHAN	HYPOTHETICAL 64.2 KD	HEXOKINASE TYPE III (3-DEHYDROQUINATE DEHY	INTERFERON ALPHA-1 PR	FOS-RELATED ANTIGEN 1
EI	VE1_HPV51	VEI_HPV26	INVO_LEMCA	VE1_HPV30	PA2R_RABIT	MGLA_HAEIN	INVO_TARBA	INVO_MOUSE	VE1_HPV31	AMO_KLEAE	AMO_ECOLI	EXOP_RHIME	TRPD_BUCAP	KAPC_ASCSU	TEF1_MOUSE	TEF1_HUMAN	YNE3_CAEEL	HXK3_HUMAN	AROD_ACTPL	INA1_PIG	FRA1_RAT
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% Query Match	67.9	707	65.4	65.4	64.1	62.8	61.5	61.5	61.5	61.5	61.5	61.5	60.3			60.3		。	59.0	59.0	59.0
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HUMAN PAPILLOMAVIRUS TYPE 26. VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.

[1] SEQUENCE FROM N.A. MEDLINE; 94265501.

1. 98e+01 1. 98e+01 2. 09e+01 3. 09e+01
CYTOCHROME P450 IIA6 ALKALINE PHOSPHATASE, REPLICATION PROTEIN E REPLICATION PROPERSOR BROYSES GYASE (CONTA SUPPRESSOR OF TOXICIT HYPOTHETICAL 13.9 KD ESS1 PROTEIN (PROCESS GLO OPERON TRANSCRIPT SESNENTATION POLARITY TRANSCRIPT TRANSCRIPTIONAL ENHAN CDC4-LIKE PROTEIN (FR TISSUE PLASMINOGEN AC PYPOTHETICAL 86.1 KD RETRROVIRUS-RELATED PO ECUYSONE-INDUCIBLE PR
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ALIGNMENTS

			•			VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.						-! - FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR DNA REPLICATION.								34;		s 0; Gaps 0;		
				-		RIDAE; PA						RED FOR I				BINDING;				Length (• • • • • • • • • • • • • • • • • • • •	2; Indels		
634 AA.	PDATE	(UPDATE)	•			PAPOVAVI						ASE REQUI				ASE; ATP-		ATP (POTENTIAL).	71684 MW; DCCE91ED CRC32;	Score 53; DB 10; Length 634;	7.11e-01	Mismatches		
PRT;	(REL. 23, CREATED)	NNOTATION			:	VIRUSES;				STEIN S.J.	•	DNA HELIC	CLEAR.	TED_CDS.		ION; HELIC		ATP (POI	i; DCCE91	Score 53;	Pred. No.	3; Mism		
STANDARD;	3, CREATE	4, LAST A	1 E1.		IS TYPE 51	TENVELOPED				, SILVERS	,225(1991)	EPENDENT	ATION: NU	T_ANNOTAI	:	REPLICATI		470	71684 MW	67.98;	54.58;	vative	ω,	
STAN					LOMAVIRU	-DNA NON		OM N.A.	303675.	RUM C.P.	5:4216-4	N: ATP-L	ULAR LOC	7; -; NC	; WIWL51	IN; DNA	TEIN.	463	634 AA;		ilarity	Conservative	stfel 34	OTFOL 12
J 1 VE1_HPV51 P26544:	01-AUG-1992 01-AUG-1992	01-OCT-1996	REPLICATION	E1.	HUMAN PAPILLOMAVIRUS TYPE 51	VIRIDAE; DS	[]]	SEQUENCE FROM N.A.	MEDLINE; 91303675.	LUNGU O., C	J. VIROL. 65:4216-4225(1991).	-!- FUNCTIO	-! - SUBCELLULAR LOCATION: NUCLEAR.	EMBL; M62877; -; NOT_ANNOTATED_CDS.	PIR; A40415; W1WL51.	EARLY PROTEIN; DNA REPLICATION; HELICASE; ATP-BINDING;	NUCLEAR PROTEIN.	NP_BIND	ы	Query Match	cals	Matches 6;	333 qhsfedstfel 343	2 QHSXQEQTFQL
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      CURR. TOP. MICROBIOL. IMMUNOL. 186:13-31(1994).
-!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR DNA REPLICATION.
-!- SUBCELLULAR LOCATION: NUCLEAR.
EMBL; X74472; G396959; -.
PIR; S36546; S36546.
EARLY PROTEIN; DNA REPLICATION; HELICASE; ATP-BINDING;
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0
                                                                                              Query Match 67.9%; Score 53; DB 10; Length 638; Best Local Similarity 46.2%; Pred. No. 7.11e-01; Matches 6; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C4-TYPE ZINC FINGERS (TWO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSÍTE; PS00031; STEROID_FINGER.
TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                      ATP (POTENTIAL). ; 6E36534F CRC32;
                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ECDYSONE-INDUCIBLE PROTEIN E78-A (DR-78).
                                                                                                                                                                                        864 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLN.
POLY-GLN.
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POLY-SER.
POLY-ASN.
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C4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                     DROSOPHILA MELANOGASTER (FRUIT FLY)
                                                                               71956 MW;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 321-433 FROM N.A.
                                                                                                                                                                                                                                                                                                       STONE B.L., THUMMEL C.S.;
CELL 75:307-320(1993).
                                                                                                                                                                                        STANDARD;
                                                                      474
                                                                                                                                  337 ehsfddatfdlsk 349
DELIUS H., HOFMANN B.;
                                                                                                                                                    OHSXQEQTFOLXK 14
                                                                               638 AA;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94060116.
                                                                                                                                                                                                                                                                                       STRAIN=CANTON-S;
MEDLINE; 94006562.
                                                                      467
                                                                                                                                                                                                                                           EIP78C OR E78A.
                                                                                                                                                                                       E78A DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZINC-FINGER
                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
                                                                      NP_BIND
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VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! FUNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO MEMBRANE PROTEINS BY TENNSCLUTAMINASE. ALL THAT RESULTS IN THE FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE. -! TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND CHER STRATITED SQUAMOUS EPITHELIA.

EMBL; M21864; G340630; --
PIR; A43733; A43733.

KERATINOCYTE; REPEAT.
                                                   POLY-ASN.
MISSING (IN TRUNCATED FORM E78B).
OLOGOCOCHOCO -> SCNSSSSTSSR (IN REF. 2).
AGMS -> VGMK (IN REF. 2).
                                                                                                                                                                                                                                                                    Gaps
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CHAN S.Y., BERNARD H.U., ONG C.K., CHAN S.P., BIRGIT H., DELIUS H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEMUR CATTA (RING-TAILED LEMUR).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                 ó
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                                                                                                                                                                                                           Score 52; DB 3; Length 864; Pred. No. 1.17e+00;
                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94265501.
DELIUS H., HOFMANN B.;
CURR. TOP. MICROBIOL. IMMUNDL. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50445 MW; BB1B0C73 CRC32;
                                                                                                                                                       5EEB72C0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 5 STANDARD; PRT; 631 AA. 0505112; 01-FEB-1994 (REL. 28, CREATED) 01-J034-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) REPLICATION PROTEIN E1.
                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 AA.
                           POLY-GLN
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486
500
554
7474
331
95865 MW;
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                                                                                                                                                                                                           66.78;
                                                                                                                                                                                                                                 Similarity 54.5%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 ggapgegelhlgk 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSENG H., GREEN H.;
CELL 54:491-496(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                  333 qhpqqqqsfgl 343
                                                                                                                                                                                                                                                                                                                                                                2 QHSXQEQTFQL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 AA;
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                       864 AA;
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  481
480
546
321
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INVO_LEMCA
P14590;
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                        DOMAIN
DOMAIN
VARSPLIC
CONFLICT
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     DOMAIN
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VENTER J.C.;
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P24711;
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                                                                                                                                             MGLA_HAEIN
        CARBOHYD
CARBOHYD
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 CARBOHYD
                            CARBOHYD
                                    SEQUENCE
                                                                                                                                                         P44884;
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 SEEFES
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J. VIROL. 66:5714-5725(1992).

-:- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR DNA REPLICATION.

-:- SOBCELLICAR LOCATION: NUCLEAR.

EMBL: X74474; G396976; --

EMBL: X96304; G333093; --

PIR: S36505; S36505

BARLY PROTEIN: DNA REPLICATION; HELICASE; ATP-BINDING;

NUCLEAR PROTEIN: DNA REPLICATION; POTENTIAL).
                                                                                                                                                                                                                                                                                                               LAMBEAU G., ANCIAN P., BARHANIN J., LAZDUNSKI M.;
J. BIOL. CHEM. 269:1575-1578 (1994).
-!- FUNCTION: MAY HAVE A KEY ROLE IN NORMAL AND PATHOLOGICAL ACTIONS
OF SECRETORY PHOSPHOLIPASE A2. ALSO BINDS TO SNAKE PA2-LIKE
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: LUNG, SKELETAL MUSCLE, BRAIN, KIDNEY AND
                                                                                                                                                                                                             01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R).
080 KCTCOLAGUS CUNICUUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
180 KD SECRETORY PHOSPHOLIPASE A2
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U03455; G456376; -. SIGNAL; REPEAT; GLYCOPROTEIN; LECTIN.
                                                                                                                     ô
                                                                                                   65.4%; Score.51; DB 10; Length 631; 53.8%; Pred. No. 1.91e+00; vative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORM)
                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 8 C-TYPE LECTIN FAMILY DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
CYS-RICH.
FIBRONECTIN TYPE-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN 1 (LONG FO
C-TYPE LECTIN 2 (LONG FO
C-TYPE LECTIN 3 (LONG FO
C-TYPE LECTIN 5 (LONG FO
C-TYPE LECTIN 5 (LONG FO
C-TYPE LECTIN 7 (LONG FO
C-TYPE LECTIN 7 (LONG FO
C-TYPE LECTIN 8 (LONG FO
                                                                         459 466 ATP (POTENTIAL).
631 AA; 71809 MW; 753395D7 CRC32;
                                                                                                                                                                                               PRT; 1458 AA.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE TISSUE-SKELETAL MUSCLE; MEDLINE; 94124484.
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POTENTIAL.
POTENTIAL.
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                                                                                                                        7; Conservative
                                                                                                                                                                                               STANDARD;
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1054
1106
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1458
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1416
1416
1258
2250
2250
2350
10938
10336
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4431
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7252
7253
                                                                                                                                        329 qhsfqdcqfelsk 341
                                                                                                                                                          2 OHSXQEQTFOLXK 14
                                                                                                                                                                                                                                                                       EUTHERIA; LAGOMORPHA.
                                                                                                              Local Similarity
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1106
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CARBOHYD
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TRANSMEM
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A VEWTER J.C.;

L. SCIENCE 269:496-512(1995).

S. CIENCE 269:496-512(1995).

C. '- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

C. '- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

C. THE TRANSPORT SYSTEM (BY SIMILARITY).

C. '- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY

C. '- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY

C. '- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY

C. EMBL: U32764; G902849; --

DR EMBL: U32764; G902849; --

DR EMBL: U32764; G902849; --

DR FRANSPORT: SOGAL TRANSPORTER.

F. PROSITE: PSOG211; ABC_TRANSPORTER.

F. PROSITE: SGGAR TRANSPORT: INNER MEMBRANE; ATP-BINDING.

F. NP_BIND

A 6 55667 MW; 8964ECA2 CRC32;
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
03-LACTOSIDE TRANSPORT ATP-BINDING PROTEIN MGLA.
MGLA OR HIGB33.
HAEMOPHILUS INFLUENZAE.
PROKARYCTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KERLAVAGE A.R., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKENDEY K., SUTTON G., FILLDS C.A., GOCANE J.D., SCOTT J.D., SHIRLEY R., LU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.K., HANNAM M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRWANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
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EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                   Score 50; DB 7; Length 1458;
Pred. No. 3.09e+00;
1; Mismatches 4; Indels
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Pred. No. 4.97e+00;
3; Mismatches 4; Indels
                                                                                      POTENTIAL.
MW; FA57C2CA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-1992 (REL. 21, CREATED)
01-WAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 AA
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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   1121 1121
1130 1130
1319 1319
1439 1439
1458 AA; 167199 M
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Local Similarity 46.2%;
les 6; Conservative
                                                                                                                                                                            Query Match 64.1%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 qpsiqdvsfelrk 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 OHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                              849 hsaheqefilsk 860
                                                                                                                                                                                                                                                                                                                                   3 HSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PASTEURELLACEAE.
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VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES.
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        755 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           757 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 31-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H(2)0(2).
-!- COFACTOR: COPPER AND TOPAQUINONE.
-!- SUBCELLULAR LOCATION: PERIPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                      464
: 71227 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          755
413
496
7554
719
83576 MW;
                                                                                                                                                                                                                                                                                                 y Match
Local Similarity 54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 50.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 gsgldgtfgvek 121
                                                                                                                                                                                                                                                                                                                                                                      327 qhsfndttfdl 337
                                                                                                                                                                                                                                                          629 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         2 QHSXQEQTFQL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 HSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496
554
556
719
755 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92210491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAOA OR IYNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOPAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 11
AMO_KLEAE
P49250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=W70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMO_ECOLI
P46883;
                                                                                                                                                                                                                                                            SEQUENCE
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BINDING
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                      DJIAN P., GREEN H.;
PROC. NATL. ACAD. SCI. U.S.A. 88:5321-5325(1991).
-!- FUNCTION: INVOLUCEIN IS A RERAITMOCYTE PROTEIN THAT FIRST APPEARS
IN THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINED TO
MEMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE
FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
-!- TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND
GTHER STRAIFIED SQUAMOUS BPITHELIA.

GTHER STRAIFIED SQUAMOUS BPITHELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOL. BIOL. EVOL. 10:1136-1149(1993).

-!- FÜNCTION: INVOLUCRIN IS A KERATINOCYTE PROTEIN THAT FIRST APPEARS
IÑ THE CELL CYTOSOL, BUT ULTIMATELY BECOMES CROSS-LINKED TO
MÉMBRANE PROTEINS BY TRANSGLUTAMINASE. ALL THAT RESULTS IN THE
FORMATION OF AN INSOLUBLE ENVELOPE BENEATH THE PLASMA MEMBRANE.
-!- TISSUE SPECIFICITY: PRESENT IN KERATINOCYTES OF EPIDERMIS AND
OTHER STRATIFIED SQUAMOUS EPITHELIA.
EMBL; LZ8819; G454419; --
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DJIAN P., PHILLIPS M., EASLEY K., HUANG E., SIMON M., RICE R.H., GREEN H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHEŖIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                           Score 48; DB 5; Length 38/;
Pred. No. 7.94e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 5; Length 467; Pred. No. 7.94e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                     387 AA; 45077 MW; 2800B15B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 AA; 54919 MW; 39DCOAFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
INVOLUCRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                PIR; A43704; A43704.
PROSITE; PSO0795; INVOLUCRIN.
KERATINOCXTE; REPEAT.
SEQUENCE 387 AA, 45077 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E1.
HUMAN PAPILLOMAVIRUS TYPE 31.
                                                                                                                                                                                                                                                                                                                                          / Match
Local Similarity 46.2%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match
Local Similarity 46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVO_MOUSE STANDARD; P48997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                 qqeaqeqelhlgk 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QHSXQEQTFQLXK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MŮSCULUS (MOUSE).
 [1] |
SEQUENCE FROM N.A.
                                                         MEDLINE; 91271381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NIH SWISS;
MEDLINE; 94104476
                                         TISSŲE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
VE1_HPV31
P17382
                                                                                                                                                                                                                                                                                                                                            ery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                   235
                                                                                                                                                                                                                                                                                                                                                                              Matches
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AC DI IN
AC DI ON
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MEDLINE; 89299478.

MEDLINE; 89299478.

MEDLINE; 89299478.

GOLDSBOROUGH M.D., DISILVESTRE D., TEMPLE G.F., LORINCZ A.T.;

VIROLOGY 171:306-3311(1989).

-1- SUBCELLULAR LOCATION: DNA HELICASE REQUIRED FOR DNA REPLICATION.

-1- SUBCELLULAR LOCATION: NUCLEAR.

FEMBL; J04533; 6459918; -.

PIR; C32444; WIML31.

PARLY PROPERN; DNA REPLICATION; HELICASE; ATP-BINDING;

NUCLEAR PROTEIN: NA REPLICATION; HELICASE; ATP-BINDING;

NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLEBSIELLA AEROGENES.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUGINO H., SASAKI M., AZAKAMI H., YAMASHITA M., MUROOKA Y.;
J. BACTERIOL. 174:2485-2492(1992).
-!- FUNCTION: ACTIVE ON TYRAMINE, TRYPTAMINE, BETA-PHENETHYLAMINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
01-MINE OXIDASE PRECURSOR (EC 1.4.3.6) (MONAMINE OXIDASE) (TYRAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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CATALYTIC BASE (BY SIMILARITY).
TOPAQUINONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                         Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 1; Length 755; Pred. No. 7.94e+00; 3; Mismatches .3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- INDUCTION: BY TYRAMINE.
-i- SIMILARITY: TO OTHER COPPER/TOPAQUINONE OXIDASES.
EMBL; D10208; G216723; -.
OXIDOREDUCTASE; COPPER; TPQ; PERIPLASMIC; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPPER (POTENTIAL).
COPPER (POTENTIAL).
COPPER (POTENTIAL).
4; 735E26ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 10;
Pred. No. 7.94e+00;
                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
DA96E287 CRC32;
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US-08-915-004-2.rsp

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   STRAIN-K12 / W3110;
AZAKAMI H., YAMASHITA M., ROH J.H., SUZUKI H., KUMAGAI H., MUROOKA Y.;
J. FERMENT. BIOENG. 77:315-319(1994).
                                                                                                                                               ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3) +
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=KIO;
MEDLINE; 96164434.
PARSONS M.R., CONVERY M.A., WILMOT C.M., YADAV K.D.S., BLAKELEY V.,
CORNER A.S., PHILLIPS S.E.V., MCPHERSON M.J., KNOWLES P.F.;
STRUCTURE 3:1171-1184(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI; RHIZOBIACEAE.
     01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 33, LAST SEQUENCE UPDATE)
01-EEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
COPPER AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (TYRAMINE OXIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
COPPER AMINE OXIDASE.
CATALYTIC BASE (PROBABLE).
TOPAQUINONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- COFACTOR: COPPER AND TOPAQUINONE.
-:- SUBUNTI: HOMODIMER.
-:- SUBUNTI: HOMODIMER.
-:- SUBULLULAR LOCATION: PERIPLASMIC.
-:- SIMILARITY: TO OTHER COPPER/TOPAQUINONE OXIDASES.
EMBL: D23670; 6804409; --
EMBL: L7571; G1000851; --
ECOGENE; EG13139; TYNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P33698:
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
SUCCINOGLYCAN BIOSYNTHESIS TRANSPORT PROTEIN EXOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K -> E (IN REF. 1).

GY -> VI (IN REF. 1).

I -> II (IN REF. 1).

MISSING (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P -> I (IN REF. 1).
A -> P (IN REF. 1).
H -> D (IN REF. 1).
7; 1223C5B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PERIPLASMIC; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 1; LA
Pred. No. 7.94e+00;
3; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    786 AA
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MEDLINE; 94042869.
GLUCKSMANN M.A., REUBER T.L., WALKER G.C.;
J. BACTERIOL. 175:7033-7044(1993).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              larity 50.0%;
Conservative
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276
288
290
456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456
659
757 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                      ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                     MAOA OR TYNA
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BINDING
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CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; ASCARIDIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                   BECKER A., KLEICKMANN A., KELLER M., ARNOLD W., PUEHLER A.;
MOL. GEN. GENTE. 241:367-379(1993).
-i- PATHWAY: EXOPOLYSACCHARIDE BIOSYNNHESIS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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TRYPTOPHAN BIOSYNTHESIS; TRANSFERASE; GLXCOSYLTRANSFERASE.
SEQUENCE 335 AA; 38099 MW; 74288035 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 48; DB 3; Length 786;
Pred. No. 7.94e+00;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 9; Length 335; Pred. No. 1.26e+01; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
ANTHRANILATE PHOSPHORIBOSYLLTRANSFERASE (EC 2.4.2.18).
                                                                                                                                                                                                                                                                                                                                                                    EXOPOLYSACCHARIDE SYNTHESIS; TRANSPORT; TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; UNCERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                    786 AA; 86123 MW; A45B9144 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 AA.
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STRAIN-1021;
MEDLINE; 94042870.
GLUCKARNIN M.A., REUBER T.L., WALKER G.C.;
J. BACTERIOL. 175:7045-7055(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%;
Similarity 30.8%;
4; Conservative
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Best Local Similarity 55.6%;
                                                                                                                                                                                                                                                        EMBL; L20758; G393241; -.
EMBL; L20758; G605655; -.
PIR; B49349; B49349.
PIR; S37031; S37031.
PIR; S39960; S39960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                MEDLINE; 94067019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 15
KAPC_ASCSU
P49673;
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TRPD_BUCAP
P42392;
                                                                                                                                STRAIN-2011
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REDUENCE FROM N.A.

MEDLINE; 96048036

RA
JUNG S., HOFFMANN R., RODRIGUEZ P.H., MUTZEL R., HOFER H.W.;

BLE EUR. J. BIOCHEM. 232:111-117(1995).

C. I GATALITIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.

C. I SHILLARITY: STRONG TWO REGULATORY CHAINS AND TWO CATALITIC.

C. I SHILLARITY: STRONG TO MAMMALIAN CATALITIC SUBUNITS.

C. I SHILLARITY: STRONG TO MAMMALIAN CATALITIC SUBUNITS.

REBL; X69806; G995969; ---

TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING; CAMP;

PROMEIN 35 43 ATP (BY SIMILARITY).

PROMEIN KINASE;

PROMEIN STRONG TO MAMMALIAN CATALITY).

PROMEIN STRONG TO STRONG TO MAMMALIAN CATALITY).

PROMEIN 35 43 ATP (BY SIMILARITY).

BINDING STRONG TO STRULLARITY).

BINDING STRONG TO STRULLARITY).

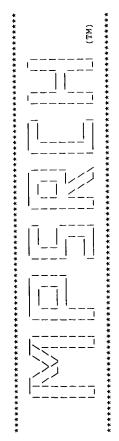
PROMEIN STRULLARITY).

BINDING STRONG TO STRULLARITY).

BINDING STRULLARITY).

PROMEIN STRULLARITY).
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                                                                                                                                                                                                                                                                                                        29 ? PROTEIN KINASE.
35 43 ATP (BY SIMILARITY).
58 58 ATP (BY SIMILARITY).
152 152 BY SIMILARITY.).
337 AA; 39171 MW; EDA30BB3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: Tue Dec 2 14:44:21 1997 Job time : 9 secs.
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1 :



Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:46:34 1997; MasPar time 2.02 Seconds 73.024 Million cell updates/sec ular output not generated.

Run on:

>US-08-915-004-3 (1-12) from US08915004.pep 94 1 XIRFLHSFTMYK 12 Description: Perfect Score: Sequence:

PAM 150 Scoring table: 101610 seqs, 12294212 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

i.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 a-geneseq28 Database:

Mean 18.812; Variance 62.835; scale 0.299 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 	<u>ب</u>	<u>~</u>	2	93	m	33	33	33	33	33	33	33	33	33	33	33	7	7	71	7	
	e-03	e-03	e-0	e-03	e-03	.77e-0	17e-0	.77e-0	54e-0	11e+0	18e+0.	18e+0	18e+0								
Pred.	5.77	5.77	7	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	5.77	9.54	2.11	5.18	5.18	5.18	
Description	nesis	Mutated OCIF, OCIF-DD	Mutated OCIF, OCIF-DD	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mutated OCIF, OCIF-DC	Mature osteoclastogen	Mutated OCIF, OCIF-CB	Mutated OCIF, OCIF-CL	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C1	Full length osteoclas	Mutated OCIF, OCIF-C2	TATA-binding protein-	bt4 Gene encoding Bt4	Lepidopteran-active t	ht4 Protoxin gene pro	
GI GI	R99923	R99940	R99941	R99939	R99937	R99936	R99938	R99924	R99948	R99942	R99934	R99932	R99935	R99931	R99925	R99933	R56496	R05420	R10129	P08200	,
DB	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	Ξ		۲ ۸	C	1
Length	12	326	327	359	359	360	360	380	393	399	401	401	401	401	401	401	1189	1165	1165	1165	1
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5.18e+01	5.18e+01	5.18e+01	8.06e+01		٠	•	1.55e+02	1.55e+02		1.92e+02	o.	2.37e+02			2.37e+02	•	m.		ო	ო.	.37	.37	.37e	2.37e+02
Incecticidal crystal	Bt4 protoxin.	Delta endotoxin.	Bacillus subtilis srf	Human melanocortin re	Sequence of a polypep	ŗ.	Conglutinin.	Bovine conglutinin.	N-heparan sulphate su	Biotin-sypthase gene	Biotin synthetase (Bi	Oncostatin M deletion	Oncostatin M subtitut	Human oncostatin M.	Luciferase mutant Tyr	ucife	Luciferase of Hotaria	Thermostable lucifera	Luciferase.	Firefly luciferase re	Vaccinia virus vector	Lux::npt-II fusion pr	Hamster sulphonylurea	Rat sulphonylurea rec
R10192	R72481	R39756	R34720	R79502	R49726	R10098	R12222	R75642	R43959	P70328	P81191	R12899	R12897	R88202	R14121	P94367	R84178	R33709	R05788	R50011	R72801	R28127	R77085	R77087
7	13	œ	7	14	σ	7	m	15	œ	~	٦	ო	٣	17	٣	Н	16	ø	'n	σ	13	Ŋ	14	14
16	1165	1165	15	325	325	578	335	371	887	331	337	223	227	252	548	548	548	548	548	550	4	815	1498	S
59.6	59.6	σ	-	57.4	\sim	55.3	54.3	54.3	54.3	53.2	53.2	52.1	52.1	52.1	52.1	7	52.1	ď	ď	a	2	2	52.1	5
26	26	26	54	54	54	52	51	51	51	20	20	6 7	6	6	49	4	49	49	6 7	4	49	49	49	49
21	22	23	24	25	26	27	28	29	30	31	3 2	i 60	34	35	36	37	38	68	40	4	42	4.3	44	4.5

ALIGNMENTS

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Mark encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 1; Page 61; 183Pp; Japanese.

Claim 1; Page 61; 183Pp; Japanese.

Claim 1; Page 61; 183Pp; Japanese.

The sequences given in R99921-23 and R99926 represent fragments of the osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PARG of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                              22-APR-1997 (first entry)
Osteoclastogenesis inhibitory factor peptide fragment #3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94; DB 20; Length 12;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                           20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-OFL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                                              Location/Qualifiers
T
R99923 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100.0%;
Local Similarity 100.0%;
Les 11; Conservative
                                                                                                                                                                                     /note= "Any amino acid" w09626217-A1.
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                                                                                                                                                                    Misc_difference 1
                                                                                                                                Homo sapiens.
                                                                                                                osteoporosis
                                                                                                                                                                                                                             29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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RESULT
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2 IRFLHSFTMYK 12 ò

RESULT

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N-PSDB; T33171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for bone resorption control, esp. treatment of osteoporosis
Claim 56; Page 113-114; 183pp; Japanese.
This Sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This Sequence represents OCIF-DDDI in which amino acids 178-252 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of OK Dunder reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto action-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                Ostepclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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23-APR-1997 (first entry)
Mutated OCIF, OCIF-DDD2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding osteoclastogenesis inhibitory factor protein - useful
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Yasuda H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Maltch 100.0%; Score 94; DB 20; Length 326; Best Local Similarity 100.0%; Pred. No. 5.77e-03; Matches 11; Conservative 0; Mismatches 0; Indels
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29-AUG-1996; 200374.
20-Epi-1996; JP-054977.
R 20-Epi-1995; JP-207508.
PR 21-JUÉ-1995; JP-207508.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
DI GOLO M, Higashio K, Kobayashi F, Mochizuki S, Mor
DI GOLO M, Shima N, Tsuda E, Ueda M, Yano K, Ya
                                                                                                                                                                                                                                                                                                                                   20-FEB-1996; JO0374.
20-FEB-1995; JD-054977.
21-JUL-1995; JD-207508.
SNOW SNOW BRAND MILK PROD CO LTD.
GCto |M, Higashio K, Kobayashi F, Mochizuki S,
Nakadawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33170.
                                                                                                                                                                                                                                                   visc_difference 198..199
/note= "Positition of deletion, delta 178-252"
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/note# "Positition of deletion, delta 253-326"
                                                                                                                                                     Location/Qualifiers
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R99940 standard; Protein; 326 AA
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                                        23-APR-1997 (first entry)
Mutated OCIF, OCIF-DDD1.
                                                                                                                                                                                                               Protein 22.326
/note= "Mature OCIF-DDD1"
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/note Mature OCIF-DDD2"
                                                                                                                                                                           1..21
"Signal peptide"
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This sequence resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (oofF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 253-326 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of the poor resorption and therefore in the control of bone resorption of incorrection and prevention of disorders of bone resorption, e.g.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR4 in which amino acids 123-164 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 100.0%; Score 94; DB 20; Length 327; Local Similarity 100.0%; Pred. No. 5.77e-03; les 11; Conservative 0; Mismatches 0; Indels
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21-JUL-1995; JP-054977.
21-JUL-1995; JP-057508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M. Higashio K, Kobayashi F, Mochizuki S, WPL; 96-402220/40.
N-PSDB; T33169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein 22.359
/note= "Mature OCIF-DCR4"
Misc_difference 143..144
/note= "Positition of deletion, delta 123-164"
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 irflhsftmyk 305
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Matches
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2 IRFLHSFTMYK 12

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis (Claim 47) Page 107-109; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR2 in which amino acids 43.84 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 40 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of disorders of bone resorption, e.g.
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Mutated OCIF, OCIF-DCR1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                         Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94; DB 20; Length 359;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
21-JUL-1995; JP-207508.
GOOD M, Higashio K, Kobayashi F, Mochizuki S, Makagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; Ţ33167.
                                                                                                                                                                                                      Misc_difference 63..64
/note= "Position of deletion, delta 43-84"
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/note= "Mature OCIF-DCR1"
Misc_difference 22..23
/note= "Position of deletion, delta 2-42"
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R99937 standard; Protein; 359 AA.
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                                             23-APR-1997 (first entry) Mutated OCIF, OCIF-DCR2.
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                                                                                                                                                                       Protein. 22.359 /note= "Mature OCIF-DCR2"
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/note= "Signal peptide"
                                                                                                                                           1..21
"Signal peptide"
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21-JUL-1995; JP-207508.
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20-FEB-1996; J00374.
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                                                                                               osteoporosis.
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Matches
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0; Gaps

Length 359;

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In rabe, 1931-09.

DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 50. Page 109-111, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of disorders of bone resorption, e.g.
                                                                                                                                           Na rabb, 1931,09.

Na encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 44; Page 105-107; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR1 in which amino acids 2-42 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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                                 Morinaga T;
Yasuda H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 94; DB 20; Length 360;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
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29-AUG-1996.

29-AUG-1996.

20-BEB-1996; JO0374.

R 20-FEB-1995; JP-054977.

PR 21-JUL-1995; JP-207508.

PA (SNOW ) SNOW BRAND MILK PROD CO LTD.

Goto M, Higashio K, Kobayashi F, Mochizuki S, Morioto M, Shima N, Tsuda E, Ueda M, Yano K, Yano M, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Tsuda E, Ueda M, Hano K, Yano M, Shima N, Tsuda E, Ueda M, Hano M, Tsuda E, Ueda M, Hano M, Tsuda E, Ueda M, Hano M, Yano M, Yano M, Shima N, Tsuda E, Ueda M, Hano M, Yano M, Y
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI, 96-402320/40.
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/note= "Mature OCIF-DCR3"

Misc_diference 105..106

/note= "Position of deletion, delta 85-122"
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Best Local Similarity 100.0%;
Matches 11; Conservative
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/note= "Signal peptide"
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Score 94; DB 20; Length 360; Pred. No. 5.77e-03;

Query Match Best Local Similarity 100.0%;

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Morinaga T; Yasuda H;

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                                                                                                                                    22-APR-1997 (first entry)
Mature osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                The encoding osteoclastogenesis inhibitory factor protein - useful for hone resorption control, esp. treatment of osteoporosis of the hone resorption control, esp. treatment of osteoporosis.

This sequence represents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-RAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone resorption and therefore in the transfer of the protein of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                   Morinaga T;
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Yasuda H;
                                                                                                                                                                                                                                                                                                              Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 94; DB 20; Length 380;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
    Indels
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0
                                                                                                                                                                                                                    29-546-1996.
20-FED-1996; J00374.
20-FED-1995; JD-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M. Higashio K, Kobayashi F, Mochizuki S, Makagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSpB; T36685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB 1996; JO0374.
21-JUL-1995; JP-054977.
21-JUL-1995; JP-054977.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M. Higashio K, Kobayashi F, Mochizuki S,
Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSPB; T33178.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                               JT |8
R99924 standard; Protein; 380 AA.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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hes 11; Conservative
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Mutated OCIF, OCIF-CBst.
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein 22.393
/note= "Mature OCIF-CBst"
Misc_difference 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note "Signal peptide"
                            331 irflhsftmyk 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irflhsftmyk 358
                                                     2 IRFLHSFTMYK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IRFLHSFIMYK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Gln371Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9626217-A1.
                                                                                                                                                                                 osteoporosis
                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoporosis
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Matches
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DNA encoding osteoclastogenesis inhibitory factor protein - useful

for bone resorption control, esp. treatment of osteoporosis

Claim 80; Page 126:128; 183pp; Japanesse.

This sequence represents a mutated version of the full length

osteoclastogenesis inhibitory factor (OCIF) of the invention. This

sequence represents a mutated version of the invention. This

sequence represents to the factor (OCIF) of the invention of the invention. This

center and amino acids 373:380 of the mature OCIF protein are deleted.

These changes are caused by the introduction of a restriction site in

the DNA encoding this protein. The OCIF of the invention has a

molecular weight by SDS-PAGE of 60 kD under reducing conditions

and 120 kD under non-reducing conditions. The protein is adsorbed onto

cation-exchangers or heparin and its activity is lowered after 10 mins

at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90

deg.C. OCIF is useful in the control of bone resorption and therefore

in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. According osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 62. Page 117-119; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CL in which amino acids 379-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-Apr-1997 (first entry)
Mutated OCIF, OCIF-CL.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                                                                                                                           Score 94; DB 20; Length 393;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94; DB 20; Length 399;
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1995; JP-054977.
21-JUL-1995; JP-054977.
SNOWN SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .T 10
R99942 standard; Protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein 22..399 //note= "Mature OCIF-CL"
                                                                                                                                                                                                                                                                                                                                                                                                                                  369 irflhsftmyk 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IRFLHSFTMYK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1996; J00374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IRFLHSFIMYK 12
                                                                                                                                                                                                                                                                                                                    393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                  osteoporosis
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23-APR-1997
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                                                                                                                                                                                                                                                                                                                    Sequence
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Morinaga T;

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On bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis folialm 38. Page 100-102, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22S in which the 27nd Gys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1997 (first entry)
Mutated OCIF, OCIF-C20S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                           Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                 Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94; DB 20; Length 401; Pred. No. 5.77e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                 20-FEB-1996; JO0374.
20-FEB-1996; JP-05497.
21-JUL-1995; JP-05497.
SNOW BRAND MILK PROD CO LTD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H 12
R99932 standard; Protein; 401 AA.
T 11
R99934 standard; Protein; 401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
                                             22-APR-1997 (first entry) Mutated OCIF, OCIF-C22S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein 22.401
/note= "Mature OCIF-C208"
                                                                                                                                                                     Protein 22..401
/note= "Mature OCIF-C225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
                                                                                                                                                        'note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IRFLHSFTMYK 12
                                                                                                                                                                                                      Misc_difference 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= C20S
WO9626217-A1.
                                                                                                                                                                                                                                     WO9626217-A1.
29-AUG-1996.
                                                                                           osteoporosis
                                                                                                                                                                                                                       /label= C22S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            osteoporosis
                            R99934;
22-APR-1997
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                                                                                                            Synthetic.
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RESULT
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Na Folds. 10310.0.

Na Folds. 10310.0.

For bone resorption control, esp. treatment of osteoporosis

Claim 41: Page 103-105; 183pp; Japanese.

This sequence represents a mutated version of the full length

Steoporosis inhibitory factor (OCTF) of the invention. This

sequence represents OCTF-C235 in which the 23rd Cys residue in the

mature OCTF protein is substituted by Ser. The OCTF of the invention

chas a molecular weight by SDS-PAGE of 60 kD under reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto

cation-exchangers or heparin and its activity is lowered after 10 mins

and 120 kD under non-reducing conditions. The protein is adsorbed onto

cation-exchangers or heparin and its activity is lowered after 10 mins

and 0.0 CTF is useful in the control of bone resorption and therefore

in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                         This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents oCIF-C20S in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A 13 R99935 standard; Protein; 401 AA. R89935. 22-APR-1997 (first entry) Mutated OCIF, OCIF. OCIF-C23S. OSteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                       DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 32; Page 96-98; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 401;
                   Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                   Length 401;
                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 20; Length 401
Pred. No. 5.77e-03;
0; Mismatches 0; Indels
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
SNOW SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
Kobayashi F, Mochizuki S,
Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94; DB 20; I
Pred. No. 5.77e-03;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 11; Conservative
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Best Local Similarity 100.0%;
Matches 11; Conservative
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/note= "Mature OCIF-C23S"
Misc_difference 400
/label= 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Signal peptide"
 Goto M, Higashio K,
Nakagawa N, Shima N,
WPI; 96-402320/40.
N-PSDB; T33162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 irflhsftmyk 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IRFLHSFTMYK 12
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                                                                                                                                                                                                                                                                                                                               osteoporosis
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                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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NA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim [29]; Page 94-96; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C195 in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                       22-AFR-1997 (first entry)
Mutated OCIF, OCIF-C19S.
Osteqclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H:
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Pred. No. 5.77e-03;
0; Mismatches 0; Indels
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
SNOW BRAND MILK PROD CO LID.
GOTO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDp; T33161.
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/note= "Mature OCIF, claim 6"
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22-APR-1997 (first entry)
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/note= "Mature OCIF-C19S"
Wisc_difference 195
/label= 717
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20-FEB-1995; JP-054977.
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This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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21-JUL-1995; JP-207508.

(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCD M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
Nakagawa N, Shima N, Isuda E, Ueda M, Yano K, Yasuda H;
NPF; 96-402320/40.
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Pred. No. 5.77e-03;
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:46:05 1997; MasPar time 2.71 Seconds 128.122 Million cell updates/sec Run on:

ular output not generated.

>US-08-915-004-3 (1-12) from US08915004.pep 94 1 XIRFLHSFTMYK 12 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

91006 seqs, 28888923 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

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1:anil 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev Mean 25.879; Variance 44.392; scale 0.583 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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F42525 #type complete A-ORF-S protein - vaccinia virus (strains WR and Copenhagen)

388 rflniyamy 396 | | | | : ::|| 3 RFLHSFTMY 11

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J. Gen. Virol. (1991) 72:1349-1376
Nucleotide sequence of 42kbp of vaccinia virus strain WR from
near the right inverted terminal repeat.
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submitted to the EMBL Data Library, July 1993
Comparative amino acid sequence analysis of Thermotoga
maritima Beta-glucosidase BglA deduced from the nucleotide
sequence of its gene indicates distant relationship between
family BGA Beta-glucosidases and other families of Beta-1
4-glycosyl hydrolases.
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Mol. Gen. Genet. (1994) 242:111-115
Comparative amino acid sequence analysis of Thermotoga
maritima beta-glucosidase (BglA) deduced from the
nucleotide sequence of the gene indicates distant
relationship between beta-glucosidases of the BGA family
and other families of beta-1,4-glycosyl hydrolases.
                                    host Homo sapiens (man) 09-Nov-1990 #text_change 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change
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#formal_name Thermotoga maritima
08 Jun-1994 #sequence_revision 10-Nov-1995 #text_change
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2; Mismatches 3; Indels
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Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoefte, H.; Soetaert, P.; Jansens, S.; Peferoen, M. Nucleic Acids Res. (1990) 18:5545
Nucleotide sequence and deduced amino acid sequence of a new Lepidoptera-specific crystal protein gene from Bacillus
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                parasporal crystal protein - Bacillus thuringiensis
#formal_name Bacillus thuringiensis
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#formal_name Methanococcus jannaschii
13 Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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#length 1160 #molecular-weight 130968 #checksum 7196
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*length 1165  #molecular-weight 132480  #checksum 8294
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3; Mismatches 1; Indels
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Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073

Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 785 - Allomyces macrogynus mitochondrion #formal_name mitochondrion Allomyces macrogynus 28-oct-1996 #sequence_revision 28-oct-1996 #text_change
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J. Mol. Biol. (1996) 255:688-701
The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence from an encestral fungus.
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Biochem. Biophys. Res. Commun. (1993) 195:866-873
Molecular cloning of a novel human melanocortin receptor.
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#formal_name Homo sapiens #common_name man
14-Jul-1994 #sequence_revision 14-Jul-1994 *text_change
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##residues 1-785 ##label PAQ
##cross-references EMBL:U41288
XY #length 785 #molecular-weight 88119 #checksum 2052
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MARX #length 322 #molecular-weight 38631
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Best Local Similarity 55.6%; Pred. No. 2.77e+01;
Tatches 5; Conservative 3; Mismatches 1;
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##cross-references EMBL:225470
##experimental_source brain
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UYPVAD #type complete noncapsid protein NSI - Aedes densovirus (strain GKV 002 002) #formal_name Aedes densovirus host Aedes aegypti (yellow fever mosquito) 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change AA0784
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#journal Virology (1991) 185:323-336
#title Mucleotide sequence and genomic organization of Aedes
densonucleosis virus.
#cross-references MUID:92024690
#accession A40784
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#domain transmembrane #status predicted #label TMI\
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#bluding_site carbohydrate (Asn) (covalent) #status predicted #label TM7\
#Bluding_site carbohydrate (Asn) (covalent) #status #length 325 #molecular-weight 36618 #checksum 589
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5R protein - human herpesvirus 6 (strain Uganda-1102)
#formal_name human herpesvirus 6
26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change
08-Apr-1994
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A33560
Lawrence, G.L.; Chee, M.; Craxton, M.A.; Gompels, U.A.;
Honess, R.W.; Barrell, B.G.
J. Virol. (1990) 64:287-299
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##cross-references GB:M28243
.X #length 772 #molecular-weight 88746 #checksum 7872
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#length 849 #molecular-weight 97542 #checksum 1776
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Pred. No. 3.89e+01;
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Best Local Similarity 55.6%; Pred. No. 3.89e+01;
Matches 5; Conservative 1; Mismatches 3; Indels
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Best Local Similarity 85.7%;
Matches 6; Conservative
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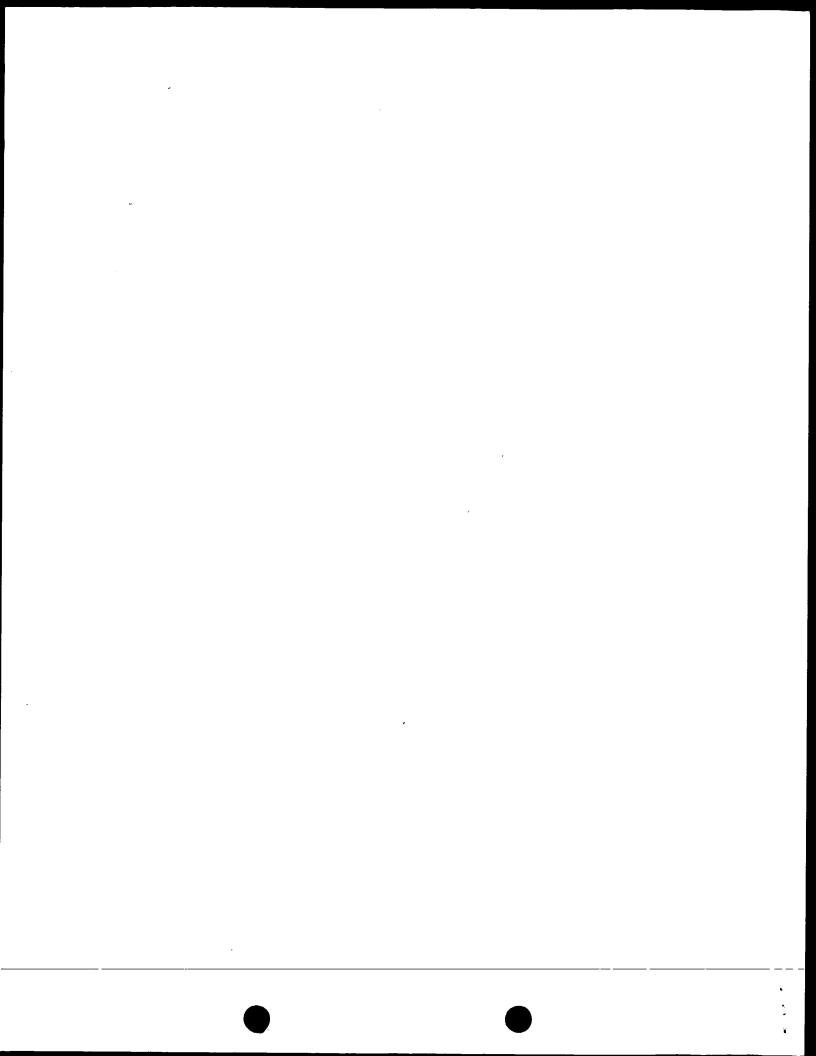
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                                                                                                                                                                                                                                                                                #authors Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; Hutchison III, C.A.; Kouzarides, T.; Martignetti, J.A.; Preddie, E.; Satchwell, S.C.; Tomlinson, P.; Weston, K.M.; Barrell, B.G. Curr. Top. Microbiol. Immunol. (1990) 154:125-169
#title Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.
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                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        this sequence was submitted to the EMBL Data Library, December 1989
                                                                                                                                          S09851 #type complete
hypothetical protein UL87 - human cytomegalovirus (strain
                   Gaps
                                                                                                                                                                                       #formal_name human cytomegalovirus, human herpesvirus 5
                                                                                                                                                                                                      host Homo sapiens (man)
07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
27-Jan-1995
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#formal_name variola virus
30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #length 941 #molecular-weight 104803 #checksum 1180
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.X #length 231 #molecular-weight 26497 #checksum 4488
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                  1; Indels
 Pred. No. 3.89e+01;
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              6; Mismatches
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Best Local Similarity 30.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative
                Conservative
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##residues 1-23
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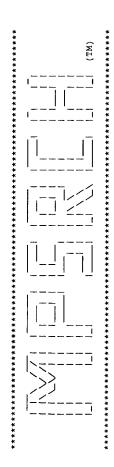
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Peakman, T.; Crouzet, J.; Mayaux, J.F.; Busby, S.; Mohan, S.; Harborne, N.; Wootton, J.; Nicolson, R.; Cole, J. Bur. J. Blochem. (1990) 191:315-323 Mucleotide sequence, organisation and structural analysis of the products of genes in the nirB-cysG region of the Escherichia coli K-12 chromosome.
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#journal Nucleic Acids Res. (1989) 17:3865-3874
#title Cloning of binding sequences for the Escherichia coli
transcription activators, FNR and CRP: location of bases
involved in discrimination between FNR and CRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S04349  #type complete
nitrate reductase (NADH) (EC 1.6.6.1) - Escherichia coli
#formal_name Escherichia coli
15-0ct-1994 #sequence_revision 15-0ct-1994 #text_change
                                               host Homo sapiens (man)
09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change
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nitrite reductase nirB - Escherichia coli
#formal_name Escherichia coli
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Nov-1995
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#length 838 #molecular-weight 92717 #checksum 1768
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F16L protein - vaccinia virus (strain Copenhagen)
#formal_name vaccinia virus
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No. 5.42e+01;
No. 5.42e+01;
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                                                                                                                                                                     Johnson, G.P. submitted to GenBank, June 1990
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                                                                                                                                                                                                                                                                                           1-231 ##label JOH
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#accession S10791
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Local Similarity 50.0%;
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Local Similarity 40.0%;
nes 4; Conservative
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##molecule_type DNA
##residues 1-839 ##label PEA
GENETICS
nirB
sumMARX
Query Match
Best Local Similarity 40.0%; Pred. No. 5.42e+01;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps. 0;
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Db 730 ikyldrfmmf 739 |::| | |: Qy 2 IRFLHSFTMY 11

Search completed: Tue Dec 2 14:46:16 1997 Job time: 11 secs.





Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:45:38 1997; MasPar time 1.94 Seconds 130.901 Million cell updates/sec Run on:

pular output not generated.

>US-08-915-004-3 (1-12) from US08915004.pep 94 Title: Description: Perfect Score:

1 XIRFLHSFTMYK 12 Sequence: 59021 segs, 21210388 residues Searched:

PAM 150 Gap 15

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 26.933; Variance 36.903; scale 0.730 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ΩI	cri	Pred. No
	59	62.8	1441	101	VGLM_BUNL7	M POLYPROTEIN PRECURS	1.41e+00
7	58	61.7	67	Ξ	YVAS_VACCV	HYPOTHETICAL 7.5 KD P	2.14e+00
m	28	61.7	790	11	YP84_CAEEL	HYPOTHETICAL 90.9 KD	2.14e+00
4	57	9.09	174	11	YRKL_BACSU		3.26e+00
S	56	59.6	446	ч	BGLA_THEMA	BETA-GLUCOSIDASE A (E	4.92e+00
9	26	59.6	1165	~	CRYS_BACTA	132 KD CRYSTAL PROTEI	4.92e+00
7	54	57.4	325	G	MC5R_HUMAN	MELANOCORTIN-5 RECEPT	1.10e+01
ω	54	57.4	772	10	UL87_HSV6U	PROTEIN US8.	1.10e+01
თ	54	57.4	775	10	UL87_HSV7J	PROTEIN U58.	1.10e+01
10	54	57.4	849	10	VNCS_AEDEV	NONCAPSID PROTEIN NS-	1.10e+01
11	54	57.4		10	UL87_HCMVA	PROTEIN UL87.	1.10e+01
12	53	56.4		10	VF16_VARV	PROTEIN F16.	1.64e+01
13	23	56.4	231	10	VF16_VACCP	PROTEIN F16.	1.64e+01
14	53	56.4	231	10	VF16_VACCC	PROTEIN F16.	1.64e+01
15	53	56.4	725	11	YDC8_SCHPO	HYPOTHETICAL 84.0 KD	1.64e + 01
16	53	56.4	847	9	NIRB_ECOLI	NITRITE REDUCTASE (NA	1.64e+01
17	53	56.4	1522	~	CIN1_LOLBL	SODIUM CHANNEL PROTEI	1.64e+01
18	52	55.3	155	æ	RECX_PSEFL	REGULATORY PROTEIN RE	2.42e+01
19	52	55.3	232	œ	RFAY_ECOLI	LIPOPOLYSACCHARIDE CO	2.42e+01
20	52	55.3	281	11	YD3B_SCHPO	HYPOTHETICAL 33.1 KD	2.42e+01
21	25	55.3	330	œ	QUTG_EMENI	QUTG PROTEIN.	2.42e+01
22	52	55.3	468	1	YL34_CAEEL	HYPOTHETICAL 53.6 KD	2.42e+01

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ALIGNMENTS

Score 59; DB 10; Length 1441; Pred. No. 1.41e+00; Query Match
Best Local Similarity 55.6%; ö

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01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL NAD(P)H OXIDOREDUCTASE IN BLITR-SPOILIC INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=168 / JH642;
KOBATSHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S.,
SATO I., TAKEUCHI M.;
SUBMITTED (MAY 1996) TO EMBL/CENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: STRONG, TO E.COLI YABF, YHER AND H.INFLUENZAE HI1544.
-!- SIMILARITY: STRONG, TO MAWMALIAN NAD(P)H DEHYDROGENASE (QUINONE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1994 (REL. 30, CREATED)
01-0CT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 31, LAST ANNOTATION UPDATE)
BETA-GLUCOSIDASE A (RC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE).
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MOL. GENET. 242:111-115(1994).
-i- CATALIYIIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
BIRL; X74163; 6395291; -.
PIR; S44570; S44570.
PIR; S41561; S41561.
PROSITE: P800572; GLYCOSYL_HYDROL_F1_1.
PROSITE: PS00533; GLYCOSYL_HYDROL_F1_2.
HYDROLASE; GLYCOSYL_HYDROL_F1_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 PROTON DONOR (POTENTIAL).
351 NUCLEOPHILE (BY SIMILARITY).
51548 MW; 0690A48B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 56; DB 1; Length 446; 50.0%; Pred. No. 4.92e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                             Indels
Best Local Similarity 50.0%; Pred. No. 2.14e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57; DB 11; I
Pred. No. 3.26e+00;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D84432; G1303711; -.
SUBTILIST; BG11778; YRKL.
HYPOTHETICAL PROTEIN; OXIDOREDUCTASE.
SEQUENCE 174 AA; 20093 MW; AD4DECD8 CRC32;
                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.6%;
Best Local Similarity 60.0%;
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STRAIN-MSB8 / DSM 3109;
MEDLINE; 94104595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 3
446 AA;
                                                                                                                  303 ikfilafsmy 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 mrflpaftgy 149
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2 IRFLHSFIMY 11
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2 IRFLHSFTMY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACILLUS SUBTILIS.
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BGLA_THEMA
Q08638;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                             P54439;
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                           ö
                              Gaps
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VACCIALA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).
VIRIDAE: DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
ORTHÓPOXVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=COPENHAGEN;
MEDLINE; 91021027.
GOBBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAİN-COPENHAGEN;
GOBBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
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                           Indels
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 90.9 KD PROTEIN CO8BIL.4 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMMS M.;
SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED 446676; G576997; --
WORLPEP: C08B11.4; CE01474.
HYPOTHETICAL PROTEIN.
SEQUENCE 790 AA; 90873 MW; 8B2A0D83 CRC32;
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                                                                                                                                                                                                                                                                                                                 01-FB-1991 (REL. 17, CREATED)
01-FB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-GCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
HYPOTHEFICAL 7.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PACLETIE:
VIROLOGY 179:517-563(1990).
EMBL; M35027; 6335532; -.
PIR; 445525; F42525.
PIR; JQ1824; JQ1824.
HYPOTHETICAL PROTEIN.
SEQUENCE 67 AA; 7503 MW; 7884D470 CRC32;
                           3; Mismatches
                                                                                                                                                                                                                                                            67 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMITH G.L., CHAN Y.S., HOWARD S.T.;
J. GEN. VIROL. 72:1349-1376(1991).
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VIROLOGY 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.7%;
50.0%;
                           5; Conservative
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Best Local Similarity
                                                                                   388 rflniyamy 396
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IRFLHSFTMY 11
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RFLHSFTMY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAİN=WR;
MEDLINE; 91259063.
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US-08-915-004-3.rsp

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3 RFLHSFTMY 11
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P24437;
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HOLLEIC ACIDS RES. 18:5545-5545[1990].
- FUNCTION: PROMOTES COLLOIDOSONOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELLAL CELLS OF MANY LEPTDOPPERAN LARVAE.
- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
- TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
- TOXIC SEGMENT OF THE PROTEIN IS PRODUCED DURING.
- OF THE SPORE COAT.
- OF THE SPO
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                                                                                                                                                                                                                                                                                                                                                                                                   BACILLUS THURINGIENSIS (SUBSP. AIZAWAI).
PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
     Gaps
                                                                                                                                                                                                                          P19415;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
132 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRIFFON N., MIGNON V., FACCHINETTI P., DIAZ J., SCHWARTZ J.C.,
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Pred. No. 4.92e+00;
3; Mismatches 1; Indels
  Indels
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MEDLINE; 93384614.
CHAJLIANI V., MIKBERG J.E.S.;
BIOCHEM. BIOPHYS. RES. COMMUN. 195:866-873(1993).
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m
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
MELANOCORTIN-5 RECEPTOR (MC5-R) (MC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 AA
  Mismatches
                                                                                                                                                                                                     PRT; 1165 AA
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5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.6%;
Similarity 60.0%;
6; Conservative
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPIENS (HUMAN)
                                                  239 vrfmhqfnny 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 vdflnsftiy 309
                                                                                                 2 IRFLHSFTMY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-HD-68;
MEDLINE; 91016842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ||:|||:|
2 IRFLHSFTMY 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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MEDLINE; 95258173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94234987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MC5R_HUMAN
P33032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOKOLOFF P
                                                                                                                                                                                                     CRYS_BACTA
                                                                                                                                                                                                                                                                                                                                                         PROTOXIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
  Matches
                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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FATHI Z., IBEN L.G., PARKER E.M.;
NEUROCHEM. RES. 20:107-113(1994).
-!- FUNCTION: RECEPTOR FOR MSH (ALPHA, BETA AND GAMMA) AND ACTH. THE
ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYIAATE CYCLASE. THIS RECEPTOR IS A POSSIBLE MEDIATOR OF THE
IMMUNOMODULATION PROPPETIES OF MELANOCORTINS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: IS EXPRESSED IN THE BRAIN BUT NOT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U58 OR 5R.
HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                  MELANOMA CELLS.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

EMBL; 225470; G397610; -.

EMBL; 127080; G435600; -.

EMBL; 008353; G522164; -.

GCRDB; GCR_0793; -.

GCRDB; GCR_0794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
PALMITATE (POTENTIAL).
PALMITATE (POTENTIAL).
R -> A (IN REF. 2).
ALPGASSARQHISM -> LCPGPALRGRGPAW (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 90080132.
LAWRENCE G.L., CHEE M., CRAXTON M.A., GOMPELS U.A., HONESS R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB 6; Length 325;
Pred. No. 1.10e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                    G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE. DOMAIN 137 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULA:
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF. 1).
F -> Y (IN REF. 2)
36600 MW; 237C436E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                           MIM; 600042; -. PROSITE; PS00337; G_PROTEIN_RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQU
01-OCT-1996 (REL. 34, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.4%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. VIROL. 64:287-299(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   61
73
73
1114
1175
1175
2233
2243
325
325
325
325
325
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325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (REL.
01-OCT-1996 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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STRAIN-BANGLADESH-1975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SANDAKHCHIEV L.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 HSFTMYK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F16L OR C20L.
VARIOLA VIRUS
                                                                                                                                                                                       PROTEIN UL87.
                                                                                                                  LT 11
UL87_HCMVA
P16730;
                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                                                                  RESULT
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                                                                                                                                                    Gaps
      MARTÍN M.E., EFSTATHIOU S., CRAXTON M., MACAULAY H.A.;
VIROLGOY 209-129-51(1995).

1: SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BCRF1,
HSV-6 U58, HVS-1 24 AND HCMV UL87.

EMBL., M68963; G325501; -.
EMBL., 833413; G854037; -.
PIR., F33560; F33560.

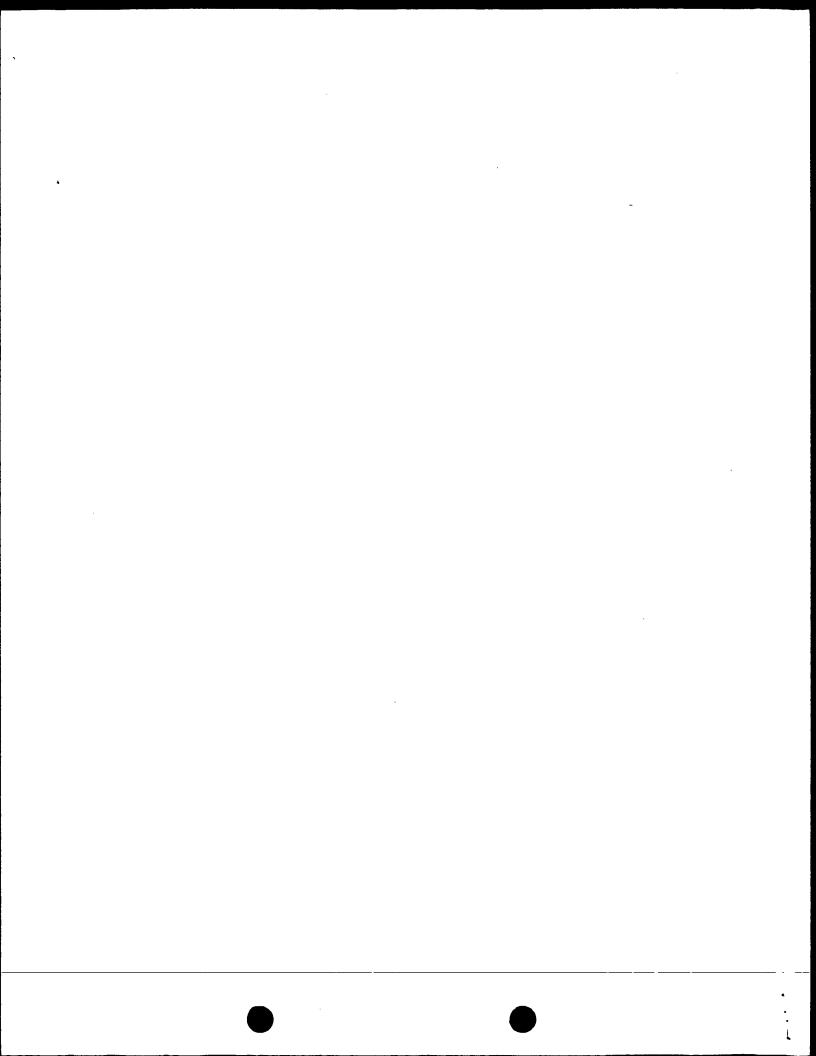
SEQUENCE 772 AA; 88746 MW; 9AD5BCIF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                       HERPES SIMPLEX VIRUS (TYPE 7 / STRAIN JI) (HHV7).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                NICHOLAS J.;
SUBMIGTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BCRF1,
HSV-6 U58, HVS-1 24 AND HCMV UL87.
EMBL, U43400; G1139661, SEQUENCE 775 AA; 89413 MW; C0C9D789 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEDES DENSONUCLEOSIS VIRUS (STRAIN GKV 002 002) (AEDES DENSOVIRUS).
VIRIDAE; SS-DNA NONENVELOPED VIRUSES; PARVOVIRIDAE; DENSOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 92024090.
MEDLINE: 92024090.
MEDLINE: 92024090.
AFANAŠIEV B.N., GALIVOV E.E., BUCHATSKY L.P., KOZLOV Y.V.;
VIROLOGY 185:323-336(1991).
-!- FÜNCTION: SEEMS NECESSARY FOR VIRAL DNA REPLICATION, PLAYS AN IMPORTANT ROLD.
IMPORTANT ROLD.
IS COVALENTLY BOUND TO THE 5'TERMINI OF VIRAL DNA, AND CAN INFLUENCE DNA PACKAGING. NS1 IS ALSO BELIEVED TO POSSESS THE TOPOISOMERASE I TYPE NICKING ACTIVITY, AND CYTOTOXIC ACTIVITY.
BIR, 440784; UTPYAD.
NOCAPSID PROTEIN, DNA REPLICATION, ATP-BINDING.
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01-AGG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1) (NCVP1).
                                                                                                                        Query Match 57.4%; Score 54; DB 10; Length 772; Best Local Similarity 85.7%; Pred. No. 1.10e+01; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 10; Length 775; Pred. No. 1.10e+01; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (POTENTIAL).
; FFC7C288 CRC32;
                                                                                                                                                                                                                                                              01-0¢T-1996 (REL. 34, CREATED)
01-0¢T-1996 (REL. 34, LAST SEQUENCE UPDATE)
10-0¢T-1996 (REL. 34, LAST ANNOTATION UPDATE)
PROTEIN US8
                                                                                                                                                                                                                                            775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    849 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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SEQUENCE FROM N.A.
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MEDLINE; 95266321
                                                                                                                                                                         470 hsfvmyk 476
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                                                                                                                                                                                             6 HSFTMYK 12
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UL87 HSV7J
P52363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ULT 10
VNCS_AEDEV
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SEQUENCE
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CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,
CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,
CHEM. T., HUTCHISON C.A. III, KONZARIDES T., MARTIGNETI J.A.,
PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.G.,
CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BCRFI,
HSV-6 U58, HYS-1 24 AND HCMV UL87.
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE; ORTHOPOXVIRUSES.
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SHCHELKUNOV S.N., BLINOV V.M., RESENCHUK S.M., TOTMENIN A.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 10; Length 941;
Pred. No. 1.10e+01;
0; Mismatches 1; Indels
    Length 849;
                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
FEBS LETI. 319:80-83(1993).
  Score 54; DB 10;
Pred. No. 1.10e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 591 POTENTIAL.
661 661 POTENTIAL.
801 801 POTENTIAL.
941 AA: 104803 MW; A9C56CC3 CRC32;
                                                                                                                                                                                                                                                                             01-AUG-1990 (REL. 15, CREATED)
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 12
VP16__VRV
VP3874;
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PROTEIN F16.
                                                    6; Mismatches
                                                                                                                                                                                                                                           941 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=INDIA-1967 / ISOLATE IND3;
MEDLINE; 93202281.
Query Match 57.4%;
Best Local Similarity 30.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.4%;
Best Local Similarity 85.7%;
Matches 6; Conservative
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                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
591
661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S09851; S09851.
                                                                                           416 vkflrnyily 425
                                                                                                                                          2 IRFLHSFTMY 11
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                                                                                                                                                                                                               Gaps
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EMBL; M35027; G335383; -. PIR: C42508; C42508.
SEQUENCE 231 AA; 26605 MW; C59DF26C CRC32;
                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
PROTEIN F16.
F16L OR F1.
VACCINIA VIRUS (STRAIN L-IVP).
VIRIDAE: DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE, 91021027.
GORBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.
PAOLETII E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VACCINIA VIRUS (STRAIN COPENHAGEN).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L.1
SEQUENCE FROM N.A.
MIKRYUKOV N.N., CHIZHIKOV V.E., PRIKHOD'KO G.G., URMMANOV I.M.,
SERPINSKII O.I., BLINOV V.M., NIKULIN A.E., VASILENKO S.K.;
BIOTEKHNOLOGIYA 4:442-449(1988).
EMBL; M57977; G335696; -.
SEQUENCE 231 AA; 26550 MW; 32D97918 CRC32;
           MASSUNG'R.F., ESPOSITO J.J., LIU L., QI J., UTTERBACK T.R., KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N., SELIVANOV N.A., CAVALLARO K.F., KERLAVACE A.R., MAHY B.W.J., VENTER C.J., NATURE 366:748-751(1993).

EMBL: X69198; G297221; ---
EMBL: X69198; G297221; ---
EMBL: L2579; G438958; ---
PIK: B36841; B36841.
SEQUENCE 231 AA; 26497 MW; 096C212B CRC32;
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                                                                                                                                                                          Query Match 56.4%; Score 53; DB 10; Length 231; Best Local Similarity 50.0%; Pred. No. 1.64e+01; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 56.4%; Score 53; DB 10; Length 231; Best Local Similarity 50.0%; Pred. No. 1.64e+01; Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
PROTEIN F16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIROLOGY 179:247-266(1990)
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                                                                                                                                                                                                                                                            3 RFLHSFTMYK 12
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MEDLINE; 94088747
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VF16_VACCP
P29892;
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P21021;
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        Length 231
    Score 53; DB 10; Length 231
Pred. No. 1.64e+01;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O1-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
HYPOTHETICAL 84.0 KD PROTEIN C25G10.08 IN CHROMOSOME I.
SPAC25G10.08
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     725 AA; 84035 MW; 56EA1958 CRC32;
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Query Match 56.4%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                           198 rfvnklkmyk 207
                                                                                                                                                                                                                            | | | : : | | | | | 3 RFLHSFTMYK 12
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YDC8_SCHPO
Q10425;
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:50:15 1997; MasPar time 8.93 Seconds 523.035 Million cell updates/sec not generated. lar output

Run on:

tle

>US-08-915-004-4
(1-380) from US08915004.pep
2861
1 ETFPPKYLHYDEETSHQLLC......QKLFLEMIGNQVQSVKISCL 380 Description: Perfect Score: Sequence:

PAM 150 Scoring table: 101610 seqs, 12294212 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq28
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21

Mean 34.473; Variance 144.575; scale 0.238 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			æ					
	ult No.	Score	Query Match	Length	DB	ΩI	Description	Pred. No.
1	: -	2861	100.0	380	20	R99924	Mature osteoclastogen	2.03e-275
	7	2861	100.0		20	R99925	Full length osteoclas	2.03e-275
	m	2847	99.5	401	20	R99931	Mutated OCIF, OCIF-C1	5.51e-274
	4	2847	99.2	401	20	R99932	OCIF,	5.51e-274
	'n	2843	99.4	401	20	R99933	Mutated OCIF, OCIF-C2	1.42e-273
	œ	2840	99.3	399	20	R99942	Mutated OCIF, OCIF-CL	2.87e-273
	7	2841	99.3	401	20	R99934	Mutated OCIF, OCIF-C2	2.27e-273
	œ	2833	0.66	401	20	R99935	Mutated OCIF, OCIF-C2	1.50e-272
	6	2794	97.7	393	20	R99948	Mutated OCIF, OCIF-CB	~i
	10	2539	88.7	360	20	R99936	Mutated OCIF, OCIF-DC	1.
	17	2537	88.7	390	50	R99357	Human tumour necrosis	3.03e-242
	12	2481	86.7		20	R99943	Mutated OCIF, OCIF-CC	1.63e-236
	13	2231	78.0	321	20	R99949	Mutated OCIF, OCIF-CS	5.85e-211
	14	2218	77.5	m	20	R99937	Mutated OCIF, OCIF-DC	1.25e-209
	15	2119	74.1	m	20	R99938	Mutated OCIF, OCIF-DC	1.60e-199
	16	2079	72.7		20	R99939	Mutated OCIF, OCIF-DC	1.94e-195
	17	1921	67.1	327	20	R99941	Mutated OCIF, OCIF-DD	2.52e-179
	80	1915	6.99	272	20	R99944	Mutated OCIF, OCIF-CD	1.03e-178
	19	1559	54.5	326	20	R99940	Mutated OCIF, OCIF-DD	1.72e-142
	20	1370	47.9	197	20	R99945	Mutated OCIF, OCIF-CD	2.53e-123

9.58e-117 8.69e-85	.05e-7	.28e-7	.52e-5	.43e-3	.43e-2	.43e-2	.28e-	1e-2	.61e-2	.61e-2	Ś	.53e-2	œ	.12e-1	43e-1	.25e-1	25e-1	Ę,	.51e-1	.59e-1	e-1	Ţ	1.14e-08
Mutated OCIF, OCIF-CB	astogenesis	enesis	Mutated OCIF, OCIF-CC	Mutated OCIF, OCIF-CP	delta53 nerve	40kD TNF inhibitor pr	p75 Tumour Necrosis F	uman TNF-R deduced	Fibroblast derived TN	ò	Sequence of a recombi	TNF-R deduced from mT	<u>-</u>	Human 75kD TNF-bindin	CD40 protein.	Myxoma virus T2 prote	virus T2 prot	Shope fibroma virus T	: fibroma	Cowpox virus T2-equiv	tumour ne	Human herpes simplex	Rat Tumour Necrosis F
R99950 R99946	32	ത	σ	σ	R77421	00	0	\vdash		R24016	001	R11142	-	160	385	786	R85072	20	86	507	580	W12659	745
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1305	928	924	695	502	405	405	401	398	398	398	390	375	366	323	301	269	269	260	260	231	223	223	206
21	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 6; Page 62-64; 183pp; Japanese.

This sequence represents the mature osteoclastogenesis inhibitory spectral (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under nonreducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                22-APR-1997 (first entry)
Mature osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 etfppkylhydeetshqllcdkcppgtylkqhctakwktvcapcpdhyytdswhtsdecl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                  Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 2861; DB 20; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.03e-275;
Matches 380; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                           20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S,
Makagawa N, Shima N, Tsuda E, Ueda M, Yano K,
 .T
R99924 standard; Protein; 380 AA.
                                                                                                                                                                                                                                                                       Nakagawa N, Shima N
WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 AA;
                                                                                                                                                                                                                                                                                                            N-PSDB; T36685
                                                                                                           osteoporosis
                                                                                                                             Homo sapiens
                                                                                                                                                           29-AUG-1996.
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RESULT
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This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl 180
                   ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfqllklwkhqn 240
                                                                            kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkygaedlektikackp 300
                                                                                                                                       22-AFR-1997 (first entry)
Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 ycspvckelgyvkqecnrthnrvceckegryleiefclkhrscppgfgvvqagtperntv 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BIFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; Nakagwa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; NN-PSDB; 136685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 401;
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Local Similarity 100.0%; Pred. No. 2.03e-275;
Nes 380; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    standard; Protein; 401 AA.
                                                                                                                                                                                                                                             qklflemignqvqsvkiscl 380
                                                                                                                                                                                                                                                             Protein 22..401
/note= "Mature OCIF, claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
/note⊨ "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkygaediektikackp 321
                                                                                        322 sdqilkllslwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhsftmykly 381
                                                                                                                                                              Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 ycspvckelqyvkqecnrthnrvceckegryleiefclkhrscppgfgvvqagtperntv 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 29; Page 94-96; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morinaga T;
Yasuda H;
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Pred. No. 5.51e-274;
0; Mismatches 1; Indels 0;
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7 29-RUG-1996, J00374.
8 20-FEB-1995, JP-064977.
7 21-JUL-1995, JP-207508.
7 21-JUL-1995, JP-207508.
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
7 And Higashio K, Kobayashi F, Mochizuki S, Mc Tsuda E, Ueda M, Yano K, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                       361 OKLFLEMIGNOVOSVKISCL 380
                                                                                                                                                                                                                                                                                                                                          22-APR-1997 (first entry) Mutated OCIF, OCIF-C19S.
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l Similarity 99.7%;
379; Conservative
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/note= "Mature OCIF-C195"
Misc_difference 195
                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide .....
/note= "Signal peptide" /note= 0.01
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 31, Page 96-98; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents oCIF-C208 in which the 20th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of disorders of bone resorption, e.g.
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                                                       142 ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl 201
121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
                                    261
                                                                                                          262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                             381
                                                                                                                                                                                                    22-APR-1997 (first entry)
Mutated OCIF, OCIF-C20S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                    ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrghssgegtfgllklwkhgn
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Yasuda H;
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Pred. No. 5.51e-274;
0; Mismatches 1; Indels 0;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
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R99932 standard; Protein; 401 AA.
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ilarity 99.7%;
Conservative
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/note= "Mature OCIF-C208"
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"Signal peptide"
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Best Local Similarity
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/label= C20S
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N-PSDB; T33162.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 3: Page 98-100, 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C21S in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. Or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1997 (first entry)
Mutated OCIF, OCIF-C21S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                     kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                           301 SDOILKLLSLWRIKNGDODTLKGLMHALKHSKTYHFPKTVTOSLKKTIRFLHSFTMYKLY 360
                                                  202 seeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfqllklwkhgn 261
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                                                                    CEEAFFRFAVPIKFIPNMLSVLVDNLPGIKVNAESVERIKRQHSSQEQIFQLLKLWKHQN
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Pred. No. 1.42e-273;
2; Mismatches 1; Indels 0;
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21-DEL-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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R99933 standard; Protein; 401
R99933;
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Best Local Similarity 99.2%;
Matches 377; Conservative
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Protein 22..401
/note= "Mature OCIF-C21S"
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 62; Page 117-119; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents orIF-CL in which amino acids 379-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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                     322 sdgilklislwrikngdgdtlkglmhalkhsktyhfpktvtgslkktirflhtftmykly 381
                                                                                                                                    262 kagdivkkiigdidlsensvgrhighanltfeglrslmeslpgkkygaediektikackp 321
                                                                                                                                                                                                                                     301 SDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                  202 ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssgegtfgllklwkhgn
142 ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestgkcgidvtl
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20-FEB-1996.
20-FEB-1996.
21-UUL-1995; UP-05497.
21-UUL-1995; UP-207508.
GOOD M. Higashio K. Kobayashi F. Mochizuki S. Makagawa N. Shima N. Tsuda E. Ueda M. Yano K. WPI: 96-403320/40.
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Pred. No. 2.87e-273;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                     R9994 2 standard; Protein; 399 AA.
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Matches 378; Conservative
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Synthetic.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 38: Page 100-102; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22S in which the 27nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchanges or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deg.C. OCIF is useful in the control of bone resorption and therefore
in the treatment and prevention of disorders of bone resorption, e.g.
241 KDQDIVKKIIQDIDLCENSVQRHIGHANLIFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
                                                                                                                                                                                     322 sdqilkllslwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhsftmykly 381
                                                                                 181 CEEAFFRFAVPIKFIPNWLSVLVDNLPGIKVNAESVERIKRQHSSQEQIFQLLKLWKHQN 240
                                                                                                                   262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                     301 SDQILKILSIWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
                                                                                                                                                                                                                                                                                                                                                                                                          Mutated OCIF, OCIF-C22S. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ycspyckelqyykqecnrthnrvceckegryleiefclkhrscppgfgvvqagtperntv 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 etfppkylhydeetshqllcdkcppgtylkghctakwktvcapcpdhyytdswhtsdecl 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                   ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrghssgegtfgllklwkhgn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morinaga 1
Yasuda H;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.27e-273;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2841; DB 20;
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                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                      361 QKLFLEMIGNOVQSVKIS 378
                                                                                                                                                                                                                                                    382 qklflemignqvqsvkis 399
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1 Similarity 99.5%;
378; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mature OCIF-C22s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 277
/label= C22S
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N-PSDB; T33164
                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis.
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22-APR-1997
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262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikaskp 321
                                                                                                                                                sdqilnllslwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhsftmykly 381
ckrcpdgffsnetsskapcrkhtncsvfgllltqkgnathdnicsgnsestqkcgidvtl
                                               ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfgllklwkhqn
                                                                                                                                                                                                            361 QKLFLEMIGNQVQSVKISCL 380
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for bone resorption control, esp. treatment of osteoporosis claim 41; Page 103-105; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C235 in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C. and is lost after 10 mins at 70 deg. C. ooff is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; DNA encoding osteoclastogenesis inhibitory factor protein - useful Yasuda H; 29-302-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-011-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33165. Location/Qualifiers JT 8 R99935 standard; Protein; 401 AA. R99935; 22-APR-1997 (first entry) Protein 22..401 /note= "Mature OCIF-C23S" Misc_difference 400 OCIF-C23S 1..21 "Signal peptide" 401 AA; Mutated OCIF, /label= C23S W09626217-A1. osteoporosis. Synthetic. osteoporosis Sednence Peptide /note= 88888888888

Length 401; Score 2833; DB 20; Pred. No. 1.50e-272; Query Match
Best Local Similarity 99.5%;
Matches 378; Conservative

etfppkylhydeetshqllcdkcppgtylkqhctakwktvcapcpdhyytdswhtsdesl 81 1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60 22 g g õ

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0; Gaps

Indels

97.7%; Score 2794; DB 20; Length 393; 99.7%; Pred. No. 1.48e-268; vative 0; Mismatches 1; Indels 0

Local Similarity 99.7%; les 371; Conservative

Matches

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Query Match

2; Indels 0; Gaps

0; Mismatches

22 etfppkylhydeetshqllcdkcppgtylkqhctakwktvcapcpdhyytdswhtsdecl 81

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DNA encoding osteoclastogenesis inhibitory factor protein - useful DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 80; Page 126-128; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CEBst in which Gln 371 is substituted by captenes represents OCIF-CEBst in which Gln 371 is substituted by the manno acids 373-380 of the mutate OCIF protein are deleted.

These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                   381
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Mutated OCIF, OCIF-CBst.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                            262 kdqdivkkiiqdidlcensvqrhighanltfeqlrslmeslpgkkygaediektikackp
                                                                                                                                                                                                                    322 sdqilkllslwrikngdqdtlkglmhalkhsktyhfpktvtqslkktirflhsftmykly
                                                                                                                                                                                                                                     241 KDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP
142 ckrcpdgffsnetsskapcrkhtncsvfgllltgkgnathdnicsgnsestgkcgidvtl
                                                                      202 ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfqllklwkhqn
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Yasuda H;
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F, Mochizuki S,
Ueda M, Yano K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-1996, 200374, 20-FEB-1996, J00374, 20-FEB-1995, JP-054997, 21-JUL-1995, JP-207508, (SNOW ) SNOW BRAND MILK PROD CO LT GOLO M, Higashio K, Kobayashi F, Nakagawa N, Shima N, Isuda E, Ue
                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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R99948 standard; Protein; 393
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                                                                                                                                                                                                                                                                                                                             361 QKLFLEMIGNQVQSVKISCL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Signal peptide"
Protein 22.393
/note= "Mature OCIF-CBst"
Misc_difference 392
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N-PSDB; T33178.
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W09626217-A1.
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Homo sapiens.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCRI in which amino acids 2-42 of the mature OCIF-protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation—exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of circums.
                            61 | XCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                             181 CEEAFFREAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN 240
                                                                                                                                                                                                                                                                                                                                                                                          202 ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfqllklwkhqn 261
                                                                                                                                                                                                                                                                                              262 kdgdivkkiigdidlcensvqrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                                                                                                                                            241 KDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutated OCIF, OCIF-DCRI.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
82|ycspvckelqyvkqecnrthnrvceckegryleiefclkhrscppgfgvvqagtperntv 141
                                                                                                 142 ckrcpdgffsnetsskapcrkhtncsvfgllltgkgnathdnicsgnsestgkcgidvtl 201
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Yasuda H;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOto M, Higashio K, Kobayashi F, Mochizuki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc_difference 22..23
/note= "Position of deletion, delta 2-42"
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Nakagawa N. Shima N.
WPI; |96-402320/40.
N-PSDB; T33166.
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23-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                            74 iefclkhrscppgfgvvgagtperntvckrcpdgffsnetsskapcrkhtncsvfglllt 133
                                                                                                                                    134 qkgnathdnicsgnsestqkcgidvtlceeaffrfavptkftpnwlsvlvdnlpgtkvna 193
                                                                                                                                                                                                                                                                                                                                   214 ESVERIKRQHSSQEQTFQLLKLWKHQNKDQDIVKKIIQDIDLCENSVQRHIGHANLTFEQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human tumour necrosis factor receptor - used to develop prods. for treating e.g. tumours, infection, auto:immune disease, graft rejection, cytocoxicity or inflammation

Claim 14; Fig 1; 59pp; English.

The receptor binds to TNF, and in particular, TNF-beta.

The receptor may be used for screening for antagonists and agonists of the receptor may be used for screening for antagonists and agonists of the receptor and for ligands for the receptor. Such agonists may be used to inhibit the growth of tumours, to stimulate cellular differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumour necrosis factor receptor.
Tumour necrosis facor; INF; receptor; INF-beta; ligand; tumour; differentiation; immune response; autoimmune disease; inflammation; septic shock; graft-versus-host; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 yhfpktvtqslkktirflhsftmyklyqklflemignqvqsvkiscl 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.7%; Score 2537; DB 20; 00.0%; Pred. No. 3.03e-242; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   versus-host reactions, and to prevent apoptosis. Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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R99357 standard; Protein; 390 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1997 (first entry)
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Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1996.
15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
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W09628546-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 96-433821/43.
N-PSDB; T35475.
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WO9626217-A1.
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                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ON encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 65; page 119-121; 183pp; Japanese.
Claim 65; page 119-121; 183pp; Japanese.
Claim 65; page 119-121; 183pp; Japanese.
This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CC in which amino acids 331-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 ckrcpdgffsnetsskapcrkhtncsvfgllltgkgnathdnicsgnsestgkcgidvtl 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 ycspyckelgyykgecnrthnrvceckegryleiefclkhrscppgfgvygagtperntv 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 etfppkylhydeetshqllcdkcppgtylkghctakwktvcapcpdhyytdswhtsdecl 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                        181 CEEAFFREAVPIKETPNWLSVLVDNLPGIKVNAESVERIKRQHSSQEQIFQLLKLWKHQN 240
                                                              202 ceeaffrfavptkftpnwlsvlvdnlpgtkvnaesverikrqhssqeqtfq11klwkhqn 261
                                                 262 kdgdivkkiigdidleensvgrhighanltfeqlrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2481; DB 20; Length 351;
Pred. No. 1.63e-236;
0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                        20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(SOLO M, Higashio K, Robayashi F, Mochizuki S,
Nakagawa M, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                                                                                     301 SDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFP 337
                                                                                                      322 sdqilkllslwrikngdqdtlkglmhalkhsktyhfp 358
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                       T 12
R99943 standard; Protein; 351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%;
Matches 330; Conservation
                                                                                                                                                                                                          23-APR-1997 (first entry) Mutated OCIF, OCIF-CC.
                                                                                                                                                                                                                                                                                                /note= "Signal peptide"
Protein 22..351
/note= "Mature OCIF-CC"
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                                                                                                                                                                                                                                                                 Synthetic.
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to the control of the control, esp. treatment of osteoporosis claim 83; Page 128-129; 183pp; Japanese.

Claim 83; Page 128-129; 183pp; Japanese.

This sequence represents a mutated version of the full length costeoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CSph in which amino acids 298-380 of the mature couls protein are replaced by Ser-Leu-Asp. These changes are caused by the introduction of a restriction site in the DNA encoding this protein.

The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
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                                                                                                                                                                                                                                                                                                                  23-APR-1997 (first entry)
Musted OCIF, OCIF-CSph.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteopocosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 0; Gaps
262 kdgdivkkiigdidloensvgrhighanltfeqIrslmeslpgkkvgaediektikackp 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding osteoclastogenesis inhibitory factor protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morinaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1995; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Makagawa N, Shima N, Tsuda E, Ueda M, Yano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 78.0%; Score 2231; DB 20; Local Similarity 100.0%; Pred. No. 5.85e-211; les 297; Conservative 0; Mismatches 0;
                                                                                                                                                         SDQILKLLSLWRIKNGDQDTLKGLMHALKH 330
                                                                                                                       322 sdqilkllslwrikngdqdtlkglmhalkh 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                          T 13
R99949 standard; Protein; 321 AA.
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"Mature OCIF-CSph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Signal peptide"
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N-PSDB; T33179.
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The coding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 47: Page 107-109: 1838p; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This mature OCIF protein are deleted. The COIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions.

To deg. Cor 30 mins at 56 deg. C, and is lost after 10 mins at 70 deg. Cor 30 mins at 56 deg. C, and is lost after 10 mins at 90 mins at 10 mins 
                                                                               Mutated OCIF, OCIF-DCR2. Octeoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 jeiefclkhrscppgfgvvqagtperntvckrcpdgffsnetsskaporkhtncsvfgll 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt tqkgnathdnicsgnsestqkcgidvtlceeaffrfavptkftpnwlsvlvdnlpgtkv\ 190}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2218; DB 20; Length 359;
Pred. No. 1.25e-209;
5; Mismatches 26; Indels 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOCO | M. Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; |96-402320/40.
                                                                                                                                                                                                                                                                                                                           difference 63..64
= "Position of deletion, delta 43-84"
                                                                                                                                                                                                 Location/Qualifiers
R999$7 standard; Protein; 359 AA.
                                                   23-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.4%;
Matches 312; Conservative
                                                                                                                                                                                                                                                                           Mature OCIF-DCR2"
                                                                                                                                                                                                                             1..21
"Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                       996; J00374
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                                                                            Mutated OCIF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T33167
                                                                                                                                                                                                                                                                                                                                                                           WO9626217-A1.
                                                                                                                                        osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                           966
                                                                                                                                                                 Synthetic.
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                            R99937
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No Fabra 13. 133.100 control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis claim 50. Rage 109-111, 183pp. Japanese.

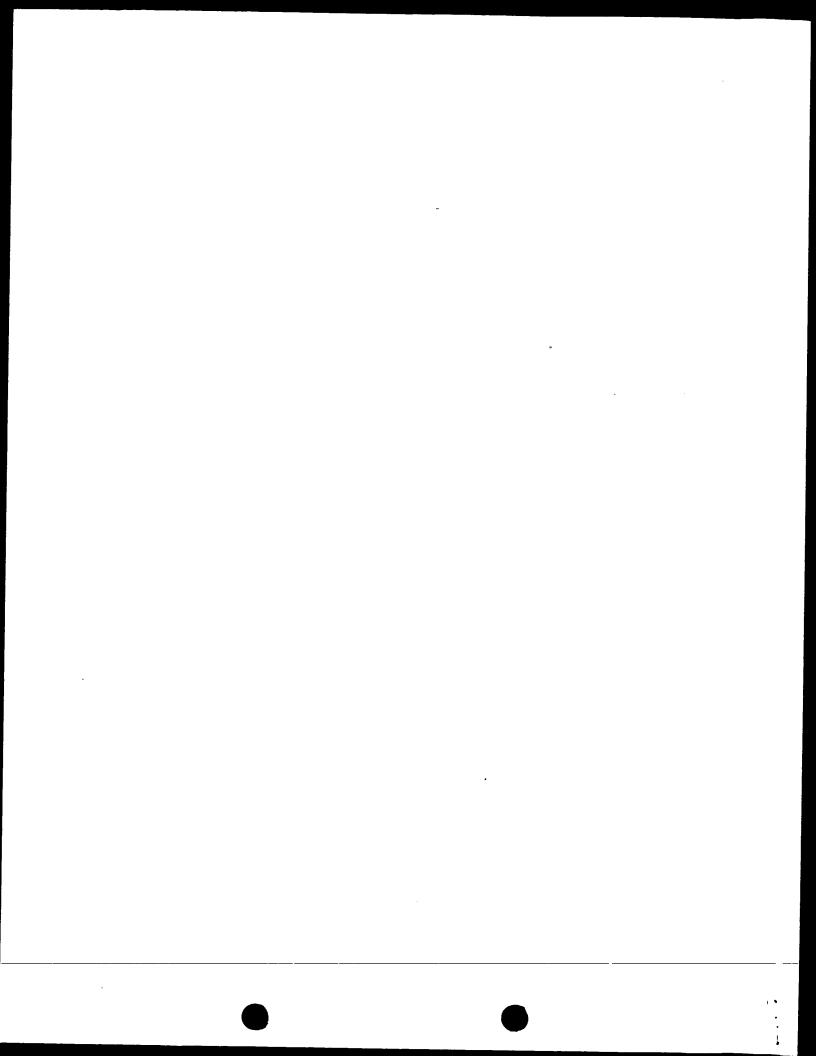
This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents of CIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto act 10 kD under non-reducing conditions. The protein is adsorbed onto at 70 deg.C or 30 mins at 56 deg.C, and its lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                            Mutated OCIF, OCIF-DCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 ceeafirfavptkftpnwlsvlvdnlpgtkvnaesverikrghssgegtfgllklwkhgn 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 38; Gaps
                                                                                                                                                                                                                                                                                         Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 89.9%; Pred. No. 1.60e-199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 ycspyckelgyvkgecnrthnrvc-------------
                                                                                                                                                                                                                                                                                 Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                Protein 22..360
/note= "Mature OCIF-DCR3"
Misc_difference 105..106
/note= "Position of deletion, delta 85-122"
                                                                                                                                                                                                                      20-FEB-1996; JO0374,
20-FEB-1995; JP-054977,
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                          Location/Qualifiers
              (first entry)
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              23-APR-1997
                                                                          Synthetic.
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Search completed: Tue Dec 2 14:51:46 1997

R99938 standard; Protein; 360 AA.

RESULT

Job time : 91 secs.



(TM)	
	* * * * * * * * * * * * * * * * * * *

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:48:32 1997; MasPar time 13.77 Seconds 797.024 Million cell updates/sec plar output not generated.

Run on:

>US-08-915-004-4 (1-380) from USO8915004.pep 2861 I ETFPPKYLHYDEETSHQLLC......QKLFLEMIGNQVQSVKISCL 380

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

91006 seqs, 28888923 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:anl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir51 Database:

Mean 46.240; Variance 103.115; scale 0.448

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	7.85e-47 3.33e-43	7.36e-43	3.73e-29	•	4.86e-25	1.41e-23	•		•	2.33e - 17	2.33e-17	3.34e-17			3.47e-15	5.33e-12	Н		1.72e-08
Description	tumor necrosis facto qene murine tumour n	tumor necrosis facto	B-cell activation pr B cell-associated su			T2 protein - rabbit	tumor necrosis facto	gene G4R protein - v	>	tumor necrosis facto	tumor necrosis facto				nerve growth factor		CD30 antigen precurs	tumor necrosis facto	CD27 antigen precurs
Ω	A35356 I48854	B38634	A50//I A46515	A46476	GOVZML	B43692	154182	S32385	D36858	157826	GOMST1	GQRTT1	JN000E	COHON	A26431	JC4302	A42086	GQHUT1	A46517
DB	6	9	17	14	~	9	13	16	ထ	14	7	7	9	7	9	14	13	7	7
Length	461	474	289	305	326	325	435	138	349	454	454	461	416	427	425	461	595	455	260
% Query Match	13.9	13.1	10.9	10.3	4.6	9.1	9.1	8.0	8.0	7.7	7.7	7.7	7.5	7.4			6.2	0.9	5.7
Score	398	375	303 294	294	269	260	260	230	230	221	221	220	215	213	207	186	178	172	162
sult No.	40	ı m·	4 N	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21

22 159 5.6 256 14 B32393 T-cell antigen 4-1BB 23 154 5.4 324 14 JC2395 Fas antigen - rat L	4.60e-08 2.33e-07 3.60e-06 1.44e-05 4.98e-05 4.98e-05 1.25e-04 1.25e-04 1.25e-04 2.48e-03 3.31e-02 1.33e-01 1.48e-01 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00 1.91e+00
159 5.6 256 14 146 5.1 271 14 141 4.9 324 14 141 4.9 255 13 140 4.9 335 13 137 4.7 250 2 134 4.7 250 2 134 4.7 250 2 134 4.7 250 2 134 4.7 250 2 134 4.7 250 2 134 13 13 124 4.3 103 8 110 3.8 310 11 115 3.6 3084 3 100 3.5 112 13 101 3.5 112 13 101 3.5 113 11 101 3.5 113 11 101 3.5 113 11 101 3.5 2677 13	Trcell antigen 4-1BB Fas antigen rat OX40 antigen precurs gene Ox40 protein - 1ymphocyte activation APO-1 antigen. Fas a apoptosis-mediating CD2 antigen precurs FAS soluble protein apoptosis-mediating SalF16R protein vacci hypothetical protein D2 protein precursor von Willebrand facto hypothetical protein intermediate filamen laminin chain A prec Fas-Delte-(4,7) protein probable membrane probable membrane probable membrane probable membrane probable membrane predesmooth hypothetical protein laminin chain A prec Fas-Delte-(4,7) protein glutamine-fructose-probable membrane pr desmoplakin I huma myosin heavy chain C
159 5.6 256 141 4.9 324 144 4.9 325 141 140 4.9 325 141 140 134 4.7 314 103 124 4.3 316 110 3.8 2813 100 3.5 110 3.5 1	B32393 CC2395 S182703 S182703 S182703 JT0752 A38142 A49053 J137383 J137383 A407036 A407036 A407036 A42523 S3427 WWHU S4142 MMMSA S6166 S5766 S5766 S5766 S5766 S6143 S6143 S6144 S6143 S6144 S6144 S6144 S6144 S6144 S6144 S6144 S666 S666
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ALIGNMENTS

T.III.S.A.	A3 tu ATE_NAMES 75 SM #f	A35356; A36475; A48416; A36007; A23666; B35010; I38094 REFERENCE A35356 #authors Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jersy, R.; Dower, S.K.; Cosman, D.; Goodwin, R.G. #iournal Science (1990) 248:1019-1023	eferen on tus ecule_	##cross-references GB:M32315 A36475 A36470. A36470. T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, #authors K.Onno, T.; Brewer, M.T.; Squires, C.H.; Thompson, R.C.; Vannice,	#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8331-8335 #title A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor. #cross-references MUID:91045991 #accession A36475 ##status preliminary ##molecule troe mRNA	idues ss-ref	#journal Cytokine (1990) 2:231-237 #title Two human TNF receptors have similar extracellular, but distinct intracellular, domain sequences. #cross-references MUID:91370690 #accession A48416 #status preliminary ##molecule_type mRNA; protein ##residues 23-461 ##label DEM ##cross-references NCBIN:63368; NCBIP:63371
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#journal J. Biol. Chem. (1900) 265:20131-20138
#title Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells.
                                                                                                                                                                                                      **residues 116-140,'P',142-195,'R',197-362,'T',364-461 ##label HEL
##cross-references GB:M35857
**NCE A23666
           #authors Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, B.; Ringold, G.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.
#cross-references MUID:90349572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Kuhnert, P.; Kemper, O.; Wallach, D.
#journal Gene (1994) 150:381-386
#title Cloning, sequencing and partial functional characterization of the 5' region of the human p75 tumor necrosis factor receptor-encoding gene (INF-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.
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#product tumor necrosis factor receptor type 2 #status
experimental #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain intracellular #status predicted #label INT.
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 461 #molecular-weight 48291 #checksum 5724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the list of introns is incomplete *superfamily tumor necrosis factor receptor type 2; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:X80021; NID:9666044; CDS_PID:9825701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##Status preliminary; translated from GB/EMBL/DDBJ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##status preliminary
##molecule_type protein
23-40;65-69;136-141;300-306 ##label LOE
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sequence extracted from NCBI backbone
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##mojecule_type protein
##residues 27-31 ##label ENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references GDB:125914
#map_position 1p36.2-1p36.2
#introns 26/3
                                                                                                                                                                                             preliminary
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63; Conservative
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164-201
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280-461
171,193
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gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
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Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834

#title Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.
#cross-references MUID:91187885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
45 yydqta-qmccskcspgqhakvfctktsdtvcdscedstytqlwnwypeclscgsrcssd 103
                                                                                                                 104 qvetqactreqnrictcrpgwycalskqegcrlcaplrkcrpgfgvarpgtetsdvvckp 163
                            97 tkqqnrvcaceagrycalkthsgscrqcmrlskcgpgfgvassrapngnvlckacapgtf 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 qmccakcppgqyvkhfcnktsdtvcadceasmytqvwnqfrtclscssscstdqvetrac 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 OLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQEC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.2%; Score 377; DB 14; Length 459;
Best Local Similarity 41.5%; Pred. No. 3.33e-43;
Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   #formal_name Mus musculus #common_name house mouse
02-uul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
148854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor necrosis factor receptor type 2 precursor - mouse #formal_name Mus musculus #common_name house mouse 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Oct-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A. Mamm. Genome (1994) 5:726-727
Allelic variation of the type 2 tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene name murine tumour necrosis factor receptor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references EMBL:X76401; NID:9433830; CDS_PID:9433831
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##cross-references GB:M60469
                                                                                                                                                                                                                          124 CPDGFFSNETSSKAPCRKHTNCSV 147
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Characterization of the promoter region of the murine p75-TNF
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               #authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
#journal Mol. Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and type 2
murine receptors for tumor necrosis factor.
#cross.references MuID:91246168
#accession A40254
                                                                                                                                                                                                                                                        Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky,
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B-cell activation protein CD40 precursor - human
B-cell surface antigen Bp50
#formal_name Homo sapiens #common_name man
03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change
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#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG4\
#length 474 #molecular-weight 50319 #checksum 7767
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EMBO J. (1989) 8:1403-1410
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Pred. No. 7.36e-43;
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##residues 1-277 ##label STA
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##cross-references EMBL:X87128
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NCE A60771
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Best Local Similarity 41.5%;
Matches 66; Conservative
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Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, D.A.
J. Immunol. (1993) 149:3921-3926
Genomic structure and chromosomal mapping of the murine CD40
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#map_position 20q12-20q13.2
KEYWORDS B-cell; glycoprotein; phosphoprotein; transmembrane protein
Biochemical characteristics and partial amino acid sequence
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#product B-cell activation protein CD40 #status
experimental #label MAT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 NRTHNRVCECKEGRY-L-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET 133
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#domain transmembrane #status predicted #label TMM\
#domain intracellular #status predicted #label CYT\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 277 #molecular-weight 30619 #checksum 6261
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#formal_name Mus musculus #common_name house mouse
18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
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##note sequence extracted from NCBI backbone

X #note #length 289 #molecular-weight 32111 #checksum
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10.6%; Score 303; DB 13; Length 277.
Local Similarity 36.8%; Pred. No. 1.19e-30;
les 56; Conservative 21; Mismatches 67; Indels
                                                                                                                 ##molecule_type_protein
##residues 21-50 ##label BRA
##experimental_source Burkitt lymphoma cell line Raji
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##residues 1-289 ##label GRI
##cross-references NCBIP:120357
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77 | NRTHNRVCECKEGRY-L--EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKELQYVKQEC 76
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#Adomain NGF receptor repeat homology #label NG3\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
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#journal Virology (1991) 184:370-382
#title Myxoma virus expresses a secreted protein with homology the tumor necrosis factor receptor gene family that contributes to viral virulence.
#cross_references MUID:91335768
                                                                                                                                                              GQVZML #type complete
T2 protein - myxoma virus (strain Lausanne)
#formal_name myxoma virus
31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
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##residues 1-305 ##label TOR
##cross-references NCBIN:75206; NCBID:75207
##note sequence extracted from NCBI backbone

** | #length 305 #molecular-weight 33617 #checksum 5203
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                                  156 slfekcypwtscedknlevlqkgtsqtnvicg 187
                                                                     134 | SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 165
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##racidues 1-326 ##label UPT
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CLASSIFICATION #superfamily mvv~~
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##residues 1-309
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Best Local Similarity
Matches 59; Conserv
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Upton, C.; DeLange, A.M.; McFadden, G. Virology (1987) 160:200-30
Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome.
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#title Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.
#accossreferences MUID:93252381
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                                                                                                         40 ctscppgsyasrlcgpgsdtvcspcknetftastnhapacvscrgrctghlsesqscdkt 99
                                                                                                                                                           20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT 79
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#formal_name Homo sapiens #common_name man
24 May-1996 #text_change
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           B43692 #type complete
12 protein - rabbit fibroma virus
#formal_name rabbit fibroma virus, Shope fibroma virus
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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#domain NGF receptor repeat homology #label NG3
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                                                          6
     Score 269; DB 2; Length 326; Pred. No. 4.86e-25;
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Pred. No. 1.41e-23;
31; Mismatches 77; Indels
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                                                       25; Mismatches 58; Indels
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                                                                                                                                                                                                                                                                                                                      159 sstetctssfnyisvefnl 177
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1larity 30.5%;
Conservative
Query Match 9.4%;
Best Local Similarity 33.8%;
Matches 47; Conservative
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Matches 51; Conser
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PEBS Lett. (1993) 319:80-83
Genes of variola and vaccinia viruses necessary to overcome
the host protective mechanisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 epghriccsrcppgtyvsakcsrirdtvcatcaensynehwnylticqlcrpcdpv-mgl 110
                                                                                                                                                                                                     111 eeiap-ctskrktqcrcqpgmfcaawalecthcellsdcppgteaelkdevgkgnnhcvp 169
                                                                                                                                                                                                                                70 OYVKOECNRTHNRVCECKEGRY----LEIEFCLKHRSCPPGFGV-VQAGTPERNTVCKR 123
                                                                                                                                                                      13 ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 HQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQE 75
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                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                       Indels 7; Gaps
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30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                           Indels 11;
                              ##cross-references GB:L04270; NID:9339761; CDS_PID:9339762 Y #length 435 #molecular-weight 46709 #checksum
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                                                                             Length 435;
                                                                                                                                                                                                                                                                170 ckaghfqntsspsarcqphtrcenqglveaapgtaqsdttc 210
                                                                                                                                                                                                                                                                                124 CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC 164
                                                                           Score 260; DB 13; L
Pred. No. 1.41e-23;
23; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 230; DB 16; L
Pred. No. 8.98e-19;
19; Mismatches 58;
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Y #length 138 #checksum 6036
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B28R protein (COP)
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##molecule_type mRNA
##residues 1-435 ##label RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-138 ##label SHC
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Best Local Similarity 35.4%;
Matches 46; Conservative
                                                                             Query Match 9.1%;
Best Local Similarity 32.3%;
Matches 52; Conservative
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                                                                                           #authors Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov, S.N.; Sandakhchiev, L.S. shchelkunov, G.N.; Sandakhchiev, L.S. submitted to the EMBL Data Library, April 1992 #description Nucleotide sequence analysis of the region of variola virus April 1901 April 1902 April 1901 Nucleotide sequence analysis of the region of variola virus
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                                 ##experimental_source strain India-1967, ssp. major, isolate Ind3
NCE
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#domain NGF receptor repeat homology #label NG3
#length 349 #molecular-weight 38189 #checksum 2016
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#length 454 #molecular-weight 50030 #checksum 4267
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##cross.references EMBL:X67117
##experimental_source strain India-1967, isolate Ind3
FICATION #superfamily NGF receptor repeat homology
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Best Local Similarity 35.4%; Pred. No. 8.98e-19;
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##cross-references GB:X69198
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##residues 1-4
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#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.

#cross-references MUID:91187885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
#journal Bur. J. Immunol. (1991) 21:1649-1656
#title Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.
#cross-references MUID:91285014
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Nucleotide sequence of the TNF type I receptor from a mouse
endothelioma cell line.
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#journal Mol-Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and type 2
murine receptors for tumor necrosis factor.
#cross-references MUID:91246168
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Immunogenetics (1991) 34:338-340
Molecular cloning and expression of the mouse Inf receptor
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                                                                                                                                                              tumor necrosis factor receptor type 1 precursor - mouse tumor necrosis factor receptor, 55K #formal_name Mus musculus #common_name house mouse 30.7un-1992 #sequence_revision 30.7un-1992 #text_change 18-oct-1996
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##cross-references GB:L26349; NID:9430732; CDS_PID:9430733
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168 - chagfflresecvpcshckkneec 191
                           123 RCPDGFFSNETSSKA-P-CRKHTNC 145
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##residues 1-454 ##label LEW
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##residues 1-454 ##label ROT
##cross-references EMBL:X57796
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tumor necrosis factor receptor type 1 precursor - rat
tumor necrosis factor binding protein 1 (TNF blocking factor)
#formal_name Rattus norvegicus #common_name Norway rat
30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
05-Apr-1995
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#product tumor necrosis factor receptor type 1 #status
predicted #label MAT\
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#product tumor necrosis factor binding protein #status
predicted #label TBP\
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#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
duplication; glycoprotein; receptor; transmembrane protein
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N #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaler, K.; Lantz, M.; Olsson, I.; Hauptmann, R.; Stratowa, C.; Adolf, G.; M.; Olsson, I.; Hauptmann, R.; Fjournal DNA Cell Biol. (1990) 9:705-715

#title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 ywhsknnsicctkchkgtylvsdcpspgrdtvcrecekgtftasgnylrgclscktcrke 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 msqveispcgadkdtvcgckengfgrylsethfqcvdcspcfng-tvtipcketgntvcn 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 LOYVK-OECNRTHNRVCECKEG---RYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                       #domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG3\
#domain reanswembrane #status predicted #label NG4\
#domain intracellular #status predicted #label NEM\
#length 454 #molecular-weight 50129 #checksum 4839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.33e-17;
21; Mismatches 65; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #binding_site carbohydrate (Asn) (covalent) #status
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##residues 1-461 ##label HIM
##cross-references GB:M63122
VI This protein is one of two known receptors for both TNF-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain transmembrane #status predicted #label MEM\
#domain intracellular #status predicted #label INT\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 -chagfflresecvpcshckkneec 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 RCPDGFFSNETSSKA-P-CRKHTNC 145
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Best Local Similarity 33.1%;
Matches 48; Conservative
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236-454
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##molecule_type mkNA
##residues 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416
##label HEU

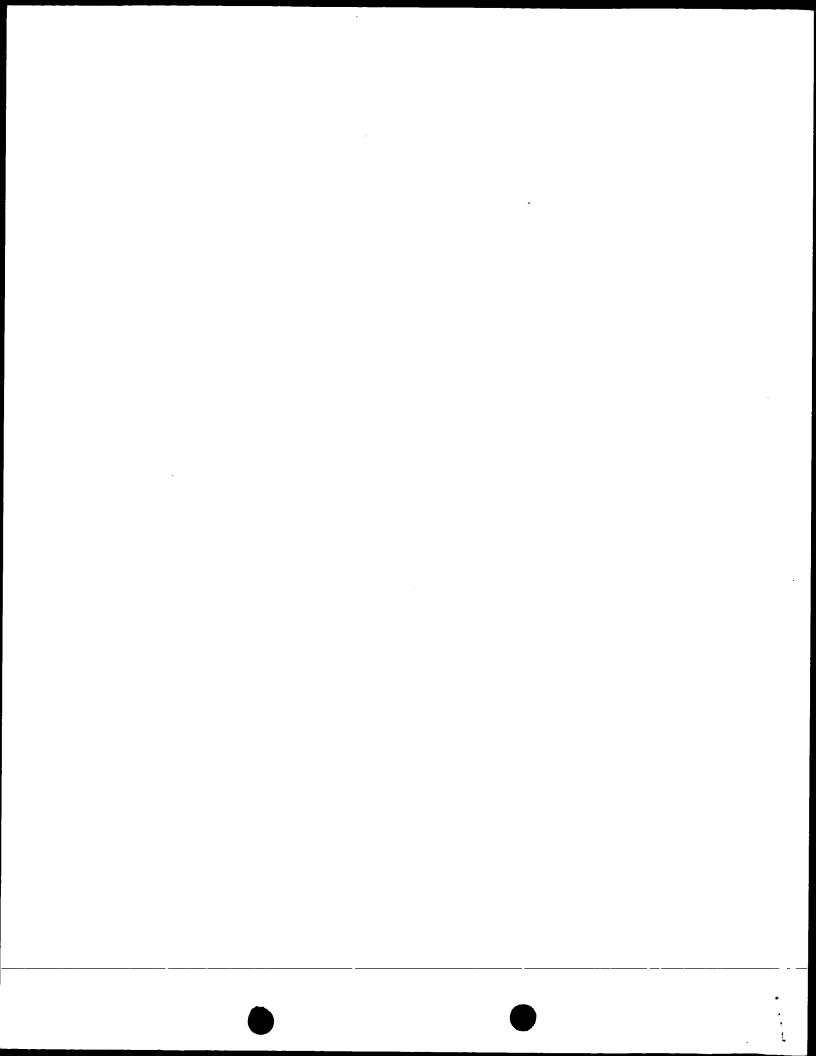
COMMENT This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells, and on a variety of nonneuronal derivatives of the neural crest.

AMENT The cysteine-rich region of the extracellular domain may form part or all of the NGF-binding site.

COMMENT This protein is thought to form a high-affinity receptor when it associates with the 140K trk proto-oncogene, which contains an intracellular tyrosine kinase domain.

CLASSIFICATION #superfamily nerve growth factor receptor; NGF receptor
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#product nerve growth factor receptor #status predicted
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M. Dev. Biol. (1990) 137:287-304
Structure and developmental expression of the chicken NGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reichardt, L.F.
#journal Neuron (1989) 2:1123*1134
#title Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system.
#cross:references MUID:90166579
                                                         Gaps 10;
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                                                                                                                                                                                                                                                        49 yahpknnsicctkchkgtylvsdcpspggetvcevcdkgtftasgnhvrgclscktcrke 108
                                                                                                                                                                                                                  109 mfqveispckadmdtvcgckknqfqrylsethfqcvdcspcfng-tvtipckekqntvcn 167
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#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                                                              10 YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JN0006 #type complete
nerve growth factor receptor, low affinity - chicken
NGF receptor
#formal_name Gallus gallus #common_name chicken
07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
JN0006; A60504
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#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#cgion serine/threonine-rich\
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Score 220; DB 2; Length 461;
Pred. No. 3.34e-17;
22; Mismatches 63; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-416 ##label LAR
##experimental source embryonic chick brain
NCE A60504
                                                                                                                                                                                                                                                                                                                                                                   123 RCPDGFF-S-NETSSKAPCRKHTNC 145
                                                                                                                                                                                                                                                                                                                                   168 -chagfflsgnectpcshckkngec 191
Query Match 7.7%;
Best Local Similarity 33.8%;
Matches 49; Conservative
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ANISM
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240-261
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                                                                                                                                            20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHTSDECLYCSPVCKELQYVKQECNR 78
                                                                              Gaps
predicted #molecular-weight 44654 #checksum 3542
                                            Length 416;
                                            Score 215, DB 6; Length 416 Pred. No. 2.01e-16; 27; Mismatches 70; Indels
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                                                                                                                                                                                                                                           154 dpclpcticeenevmvke-ctatsdaec 180
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                                            y Match 7.5%;
Local Similarity 30.4%;
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:47:03 1997; MasPar time 9.74 Seconds 827.678 Million cell updates/sec ular output not generated.

Run on:

>US-08-915-004-4 (1-380) from US08915004.pep 2861 Description: Perfect Score: Title:

1 ETFPPKYLHYDEETSHQLLC......QKLFLEMIGNQVQSVKISCL 380 Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

swiss-prot34 Database:

1:pait1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 Mean 48.034; Variance 81.732; scale 0.588 Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	6.30e-63	3.56e-56	2.64e-40	2.31e-38	5.03e-33	3.52e-32	3.98e-31	3.98e-31	6.59e-25	4.45e-23	7.09e-23	7.20e-22	1.81e-21	2.85e-20	1.51e-16	3.67e-16	1.24e-14	1.67e-13	4.22e-11	4.22e-11	8.91e-09	2.00e-08	
	Description		FACTOR	RECEPTOR PRECUR	RECEPTOR PRECUR	TUMOR NECROSIS FACTOR	LYMPHOTOXIN-BETA RECE	TUMOR NECROSIS FACTOR	LYMPHOTOXIN-BETA RECE	PROTEIN C22/B28 HOMOL	TUMOR NECROSIS FACTOR	TUMOR NECROSIS FACTOR	LOW-AFFINITY NERVE GR	LOW-AFFINITY NERVE GR	LOW-AFFINITY NERVE GR	FASL RECEPTOR PRECURS	TUMOR NECROSIS FACTOR	CD30L RECEPTOR PRECUR	TUMOR NECROSIS FACTOR	4-1BB LIGAND RECEPTOR	CD27L RECEPTOR PRECUR	OL RECEPTOR	OX40L RECEPTOR PRECUR	
	ΔI	TNR2_HUMAN	TNR2_MOUSE	CD40_HUMAN	CD40_MOUSE	VT2_MYXVL	TNRC MOUSE	VT2_SFVKA	TNRC_HUMAN	VC22_VARV	TNR1_MOUSE	TNR1_RAT	NGFR_CHICK	NGFR HUMAN	NGFR RAT	FASA_BOVIN	TNR1_PIG	CD30_HUMAN	TNR1_HUMAN	41BB MOUSE	CD27_HUMAN	OX40_RAT	OX40_MOUSE	
	DB	6	σ	7	7	10	σ	10	σ	10	σ	σ	9	ø	9	m	6	7	σ	Н	7	^	7	
	Match Length	461	474	277	289	326	415	325	435	349	454	461	416	427	425	323	461	595	455	256	260	271	272	
as 0	Match	14.2	13.1	10.6	10.3	4.6	6	6	9.1	0.8	7.7	7.7	7.5	7.4	7.2	9.9	6.5	6.2	9	5.6	5.6	5.1	5.0	
	Score	405	375	303	294	269	265	260	260	230	221	220	215	213	207	188	186	178	172	159	159	146	144	
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4-1BB LIGAND RECEPTOR	OX40L RECEPTOR PRECUR	FASL RECEPTOR PRECURS	CD27L RECEPTOR PRECUR	FASL RECEPTOR PRECURS	PROTEIN A53.	PROTEIN A53.	HYPOTHETICAL 41.6 KD	CAMP-REGULATED D2 PRO	VON WILLEBRAND FACTOR	LAMININ ALPHA-1 CHAIN	GLUCOSAMINE FRUCTOSE	HYPOTHETICAL 128.8 KD	DESMOPLAKIN I AND II	PUTATIVE TRANSLATIONA	PHOSPHATE REGULON SEN	PRE-MRNA SPLICING FAC	VALYL-TRNA SYNTHETASE	CHROMOSOME ASSEMBLY P	PROBABLE SERINE/THREO	MYOSIN HEAVY CHAIN C	BASEMENT MEMBRANE-SPE	O MINING WINGH WEGING	DYNEIN HEAVI CHAIN, C
41BB_HUMAN	OX40_HUMAN	FASA MOUSE	CD27 MOUSE	FASA_HUMAN	VA53 VACCC	VA53 VACCV	YIH9 YEAST	D2 DICDI	VWF_HUMAN	LMA1 MOUSE	GFA1 CANAL	YG3C_YEAST	DESP HUMAN	YAO5 SCHPO	PHOR SHIDY	PR31 YEAST	SYV YEAST	XCPE XENLA	KAB7 YEAST		PCBM MOUSE		DYHC_YEAST
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ALIGNMENTS

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SEQUENCE FROM N.A.
MEDILINE; 90260639.
SMITH C.A., DAVIS I., ANDERSON D., SOLAM L., BECKMANN M.P., JERZY R.,
DOWER S.K., COSMAN D., GOODWIN R.G.;
SCIENCE 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362. MEDLINE; 91056048. L.COTSCHER H., SCHLAEGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W., BROCKHAUS M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93016040.
PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,
LIPARI M.T., GOEDDEL D.V.;
                                      01-806-1991 (REL. 17, CREATED)
01-806-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-807-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-807-1995 (REL. 32, LAST ANNOTATION UPDATE)
UNDOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B).
                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                        KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W., HALE K.K., SQUIRES C.H., THOMPSON R.C., VANNICE J.L.; PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 90349572.
HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D., RINGOLD G.M.;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).
           461 AA
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J. BIOL. CHEM. 265:1531-1536(1990).
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           PRT;
           STANDARD;
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                                                                                                                          TNFR2 OR TNFBR
          TNR2_HUMAN P2033;
RESULT
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SAPIENS (HUMAN)
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CD40_HUMAN
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       yydqta-qmccskcspgqhakvfctktsdtvcdscedstytqlwnwvpeclscgsrcssd 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 ADEETSHQILCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6.30e-63;
26; Mismatches 59; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR 2. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNR2_MOUSE STANDARD; PRT; 474 AA.
P25119;
01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (INF-R2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 405; DB 9; Length 461;
                                                                                                                                                                                                                                                      PROSIȚE; PS00652; TNFR_NGFR.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capgtfsnttsstdicrphqicnvvai---p-gnasrdavctsts 204
                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R -> P (IN REF. 3).

R -> M (IN REF. 1).

A -> T (IN REF. 3).

OF5DOC44 CRC32;
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TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                              4 X INFR-CYS.
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
BJOL. CHEM. 267:21172-21178(1992).
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Conservative
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196
363
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143
161
161
171
193
                                                                                                                                                A35356; A35356.
A36007; A36007.
A36475; A36475.
B35010; B35010.
A23666; A23666.
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67
75
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196
363
461 AA;
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les | 69; Conserv
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MIM; 191191;
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TRANSMEM
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CONFLICT
SEQUENCE
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REPEAT
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PIR;
PIR;
PIR;
PIR;
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P25942;
01-MAY-1992 (REL. 22, CREATED)
01-TAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-TAY-1994 (REL. 29, LAST ANNOTATION UPDATE)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (RPS0) (CDM40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 gmccakcppggyvkhfcnktsdtvcadceasmytgvwngfrtclscssscttdgveirac 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 tkgqnrvcaceagrycalkthsgscrqcmrlskcgpgfgvassrapngnvlckacapgtf 171
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Pred. No. 3.56e-56;
21; Mismatches 61; Indels 11; Gaps
                                                                                                                                                                                         MEDLINE; 91246168.

MEDLINE; 91246168.

GOODMIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
COPELAND N.G., JENKINS N.A., SMITH C.A.;
MOL. CELL. BIOL. 11:3020-3026(1991).
-!- FUNCTION: RECEPTOR FOR TNF-ALPHA.
-!- SUBCELDULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR RECEPTOR 2.
                                                         SECUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.
WONG G.H., CHEN E.Y., GOEDDEL D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P19438; 1TNR.
PROSITE; PS00652; TNFR_NGFR.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
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17. DC32B2B6 CRC32;
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TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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Local Similarity 41.5%;
les 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                      EMBL; M60469; G199828; -. EMBL; M59378; G202095; -. PIR; B38634; B38634.
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163
181
69
195
                       EUTHERIA; RODENTIA.
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474 AA;
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7;

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DOMAIN
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P27512;
01-A02 (REL. 23, CREATED)
01-CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SINGLELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- ISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; X60592; G29851; -.
PIR; S04460; S04460.
PIR; S04460; S04460.
PROSITE: PS00652; TWFR NGFR.
RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                  SEQUENCE FROM N.A.
MEDLINE; 89356608.
AFABNINOVIC I., CLARK E.A., SEED B.;
EMBO J. 8:1403-1410(1989).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BABA/C; TISSUE-LIVER;
MEDIINE: 93094588.
GRIMALDI J.C., TORRES R., KOZAK C.A., CHANG R., CLARK E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 303; DB 2; Length 277; Pred. No. 2.64e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/C;
TORRES R.M.;
SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3B284411 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 safekchpwtscetkdlvvqqagtnktdvvcg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 SSKAPCRKHINCSVFGLLLTQKGNATHDNICS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFR-CYS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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TORRES R.M., CLARK E.A.;
J. IMMUNOL. 148:620-626(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30619 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
153
180
277 AA;
                               EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
REVISIONS.
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DOMAIN
REPEAT
REPEAT
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REPEAT
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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96 taesdtvctckegghctskdceacaghtpcipgfgvmematettdtvchpcpvgffsngs 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 cdlcqpgsrltshctalektqchpcdsgefsaqwnreirchqhrhcepn-qglr-vkkeg 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CDKCPPGIYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKELQYVKQEC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 91335768.

MEDLINE: 91335768.

UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;

VIROLOGY 184:370-382(1991).

-!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS INF TO REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL ANTIVIRAL EFFECTS OF THE CYTOKINE.

-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

EMBL; M95181; G322310; -.

EMBL; M95182; E199442; -.

PIR; A05566; GQZZML.

HSSP; P19438: ITNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Gaps
HOWARD M., COCKAYNE D.A.;

J. IMMUNOL. 149;3926,1992).

J. IMMUNOL. 149;3926,1992).

J. IMMUNOL. 169;3926,1992).

J. SECEPTON RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.

J. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROFEIN.

J. SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

EMBL; M94128; G192526; JOINED.

EMBL; M94128; G192526; JOINED.

EMBL; M94127; G192526; JOINED.

EMBL; M94127; G192526; JOINED.

EMBL; M94127; G192526; JOINED.

EMBL; M94127; G192526; JOINED.

PIR; A46476; A46476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYXOMA VIRUS (STRAIN LAUSANNE).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                        PROSITE; PS00652; TNFR_NGFR.
RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR'(PROTEIN T2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 294; DB 2; Length 289
Pred. No. 2.31e-38;
20; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                      CD40L RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X INFR-CYS.
INFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D8D70A2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN T2.
4 X INFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 slfekcypwtscedknlevlqkgtsgtnvicg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00652; INFR_NGFR.
GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match
Local Similarity 38.8%;
hes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
326
186
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2194
2194
216
255
1061
1104
1185
289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEPORIPOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 5
VT2_MYXVL
P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PR
                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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DOMAIN
REPEAT
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REPEAT
REPEAT
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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W.
                                                                          9.3%;
ilarity 28.9%;
Conservative
                                                           44956
                                                                                                                                                                                                                                                           STANDARD;
    124
132
150
169
187
179
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186
104
104
1186
1186
1181
1205
238
                                          40
179
115 AA;
                                                                                   Local Similarity
                                                                                                                                                                                                          231 vlfllft 237
                                                                                                                                                                                                                         183 EAFFRFA 189
                                                                                                                                                                                                                                                         VT2_SFVKA
P25943;
                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
          DISULFID
                   DISULFID
                                           CARBOHYD
                                                  CARBOHYD
                                                           SEQUENCE
                                                                            Query Match
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL; U20173; G801621; -.
EMBL; U30798; G1061327; -.
                                                                                                                                               100 rdrvcdcsagnycllkgqegcricapktkcpagygvs-ghtrtgdvlctkcprytysdav 158
                                                                                                                                                           20 | CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT 79
                                                                                                                  40 ctscppgsyasrlcgpgsdtvcspcknetftastnhapacvscrgrctghlsesgscdkt 99
                                                                                                  9; Gaps
                                                                                                                                                                                                                                                                                                                               STRAİN=CVB; TISSUE-LUNG;
FORCE W.R., WILLIAMS-ABBOTI L., BROWNING J., HESSION C., TIZARD R.,
                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                 Length 326;
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96163885.
NAKAMURA T., TASHIRO K., NAZAREA M., NAKANO T., SASAYAMA S.
                                                                                         Pred. No. 5.03e-33;
25; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
LYMPHOTOXIN-BETA RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U30798; G1061327; -.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                 DB 10;
                                                                 2F059A61 CRC32;
                                                                                                                                                                                                                                               01-0¢T-1996 (REL. 34, CREATED)
01-0¢T-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0¢T-1996 (REL. 34, LAST ANNOTATION UPDATE)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                 415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
TWFR-CYS 1.
TWFR-CYS 3.
TWFR-CYS 3.
TWFR-CYS 4.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                  Score 269;
                                                                  35208 MW;
                                                                                                                                                                                               134 SSKAPCRKHTNC-SV-FGL 150
                                                                                                                                                                                sstetctssfnyisvefnl 177
                                                                                 Query Match
Best Local Similarity 33.8%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               HONJO T.;
GENOMICS 30:312-319(1995).
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
415
223
2223
2244
415
2113
2113
58
80
98
116
 62
1104
1147
1186
66
1181
205
238
                                        181
205
238
326 AA;
                                                                                                                                                                                                                                                                                                        EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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31
224
245
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TNRC MOUSE
                                        CARBÓHYD
CARBÓHYD
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TRANSMEM
                                                                 SEQUENCE
                                 CARBOHYD
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REPEAT
REPEAT
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**A MEDLINE;
**SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,

**A MCRADDEN G., GOODWIN K. G.;

**B MCRADDEN G., GOODWIN K. G.;

**A MCRADDEN G., GOODWIN K. G.;

**I BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).

**C -1- FUNCTION: BINDS TO INF-ALPHA AND BETA. PROBABLY PREVENTS THE TO

**REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL

**A MILLAR LIYE. COMPAINS A LA-NGFR/THFR-TYPE CYSTEINE-RICH REGION.

**DR EMBL, M7433; -; NOT_ANNOTATED_CDS.**

**DR EMBL, A37272; 1819408; -

**DR PIR; B43692; B43692.

**DR PIR; B43692; B43692.

**DR PROSITE; PSO0652; TNFR. NGFR.**

**PROSITE; PSO0652; TNFR.**

**PROSITE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE STONE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 epmhdvccsrcppgefvfavcsrsqdtvcktcphnsynehwnhlstcqlcrp-cdivlgf 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 eevapctsdrkaecrcqpgmscvyldnecvhceeerlvlcqpgteaevtdeimdtdvncv 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 VK-QECNRTHNRVCECKEGR---YLEIE--FCLKHR-S-CPPGFGV-VQAGTPERNIVCK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 pckpghfqntssprarcqphtrceigglveaapgtsysdticknppepgamlllaillsl 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 RCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTLCE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHISDECLYCSPVCKE-LQY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
LEPORIPOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (REL, 22, CREATED)
01-MAY-1992 (REL, 22, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL, 28, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Mismatches 92; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 265; DB 9; Length 415; Pred. No. 3.52e-32;
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
3C5DD121 CRC32;
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
PROTEIN T2.
4 X INFR-CYS.
INFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
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MEDILINE; 87321103.
UPTON C., DELANGE A.M., MCFADDEN G.;
VIROLOGY 160:20-30(1987).
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                                                                                                                             100 hdrvcncstgnycllkgqngcricapqtkcpagygvs-ghtragdtlcekcpphtysdsl 158
                                                                                 20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT 79
                                                                   40 caschpgfyasrlcgpgsntvcspcedgtftastnhapacvscrgpctghlsesqpcdrt 99
                                                                                                                                                                                                                                             P36941:
01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 24, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94225209.
COME PD., VAN ARSDALE T.L., WALTER B.N., WARE C.F., HESSION C., ELRENFELS B., BROWNING J.L., DIN W.S., GOODWIN R.G., SMITH C.A.; SCIENCE 264:707-710(1994).
-:- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMUNE DEVELOPMENT.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
EMBL: L04270; G339762: -.
                                                                                                                                                                                                                                                                                                                                                                                                                BAENS M., CHAFFANET M., CASSIMAN J.J., DEN BERGHE H., MARYNEN P.;
GENOMICS 16:214-218(1993).
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                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                       Length 325;
                                            Indels
                                                                                                                                                                                      134 SSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
                                                                                                                                                               sptercgtsfnyisvgfnlypvnetscttt-aghneviktkeftvtl 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYMPHOTOXIN-BETA RECEPTOR EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P19999; ICLG.
PROSITE; PS00652; TNFR_NGFR.
RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                             31; Mismatches 77;
                    Query Match 9.1%; Score 260; DB 10; Best Local Similarity 30.5%; Pred. No. 3.98e-31; Matches 51; Conservative 31; Mismatches 77;
325 AA; 35132 MW; C9D2C87B CRC32;
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TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                     STANDARD;
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2111
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228
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980
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TISSUE=LIVER;
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                                                                                                                                                                                                                       RESULT 8
TNRC_HUMAN
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DOMAIN
TRANSMEM
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CARBOHYD
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SEQUENCE
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                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                               SHCHELKUNOV S. N., BLINOV V.M., SANDAKHCHIEV L.S.;
FEBS LETT. 319:80-83(1993).
-!- SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
EMBL, X69198; G457087; -.
EMBL, X67117; G516449; -.
PIR, 1946888, D36888.
PIR, 546888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 cntthnricecspgyycllkgssgckacvsqtkcgigygvs-ghtsvgdvicspcgfgty 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 CNRTHNRYCECKEGRY--LE--IE--FCLKHRSCPPGFGVVQAGTPERNTYCKRCPDGFF 129
                                                                                                                                                                                                                                                                              13 ETSHOLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 hnlcclscppgtyasrlcdsktntqctpcgsgtftsrnnhlpaclscngrcnsnqvetrs 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIOLA VIRUS.
VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;
                                                                                      Score 260; DB 9; Length 435;
Pred. No. 3.98e-31;
23; Mismatches 75; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 10; Length 349; 6.59e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 ckaghfqntsspsarcqphtrcenqglveaapgtaqsdttc 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 108 2 X TNFR-CYS.
31 66 TNFR-CYS 1.
67 108 TNFR-CYS 349 AA, 38189 MW, 500B435 CRC32;
   177 177 POTENTIAL.
435 AA; 46709 MW; 203B82DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches
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01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 230;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE; 93202281.
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35.4%;
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                                                                                             9.1%;
                                                                                                                       Local Similarity 32.3%;
nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN C22/B28 HOMOLOG.
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VC22_VARV
P34015;
CARBOHYD
SEQUENCE
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M GENTE DATE OF ALL MEDITAL 30.165-175(1993).

I. MOTHE J., BLUETHHANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;

MOL IMMUNOL. 30.165-175(1993).

I. STRUCTION RECEPTOR FOR THE ALLPHA

I. STRUCTION RECEPTOR FOR THE ALLPHA

I. STRUCTION RECEPTOR FOR THE ALLPHA

I. STRUCTION RECEPTOR FOR THE ALLPHA

I. STRUCTULAR LOCATION: TYPE I MEMBRANE PROTEIN.

I. STRUCTULAR LOCATION: TYPE I MEMBRANE PROTEIN.

I. STRUCTULAR LOCATION: TYPE I MEMBRANE PROTEIN.

IR EMBL; MS9377; G1020207; - .

EMBL; MS9377; G1020207; - .

EMBL; MS9676; G202102; - .

EMBL; MS9667; G202102; J0INED.

IR MBL; MS9677; G202102; J0INED.

IR MBL; MS9677; G16677;

IR S19677; S16677.

IR S19677; S16677.

IR RSSIPP, P19438; ITNR.

IR SSSIPP; P550017; DEATH_DOWAIN.

IR RECEPPOR; TRANSEMBRANE, GLYCOROTEIN; REPEAT; SIGNAL.
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (INF-R1) (P55).
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 91285014.
BARRETT K. FELDRANN M., FOXWELL B.M.J.;
GRAY P.W., FELDRANN M., FOXWELL B.M.J.;
EUR. J. INMUNOL. 21:1649-1656(1991).
                                            MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR RECEPTOR 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 91246168.
GOODWIN N.G., ADERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
COPELIAND N.G., ADENKINS N.A., SMITH C.A.,
MOL. CELL. BIOL. 11:3020-3026(1991).
                                                                                                      SEQUENCE FROM N.A.
MEDLINE: 91187885.
LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
WONG G.H., CHEN E.Y., GOEDDEL D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X INFR-CYS.
TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-SPLEEN,
MEDLINE; 92039915.
ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
IMMUNGGENETICS 34:338-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
SIMILARITY.
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TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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IMMUNOGENETICS 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                 OR TNFR-1
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DOMAIN
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DOMAIN
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DISULFID
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REPEAT
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REPEAT
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MEDLINE; 91090841.

A HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
HIMMLER A., OLSSON I., HADPMANN R., STRATOWA C., ADOLF G.R.;
DNA CELL BIOL. 9:705-715,1990.

- I- FUNCTION: RECEPTOR FOR TNF-ALPHA.

- I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- I- SIMILARIY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

REMBL; M63122; G207362; -

- REMBL; M63122; G207362; -

RESP: P19438; 11NR.

R PROSITE; PS00652; TYRE LOFR.

R PROSITE; PS0017; DEATH_DOMAIN.

R RECEPTOR: TRANKEMBRARA; GLYCOPROTEIN; REPEAT; SIGNAL.
                                                                                                                                                                         <u>.</u>
ن
                                                                                                                                                                                                                                   109 msqveispcqadkdtvcgckenqfqrylsethfqcvdcspcfng-tvtipcketqntvcn 167
                                                                                                                                                                                            49 yvhsknnsicctkchkgtylvsdcpspgrdtvcrecekgtftasqnylrqclscktcrke 108
                                                                                                                                                                                                                                                        69 LOYVK-QECNRTHNRVCECKEG --- RYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                       10 YDEETSHQLLCDKCPPGTXLKQHCTAK-WKIVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
                                                                                                                                                                     21; Mismatches 65; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                             01-AGG-1991 (REL. 19, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (INF-R1) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR RECEPTOR 1. EXTRACELLULAR (POTENTIAL).
                                                                                                                                               Score 221; DB 9; Length 454;
Pred. No. 4.45e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                   R -> G (IN REF. 6).
4B6EEC09 CRC32;
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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                                                                                                                                                                                                                                                                             168 -chagfflresecvpcshckkneec 191
  50129 MW;
                                                                                                                                                Match 7.7%;
Local Similarity 33.1%;
les 48; Conservative
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454 AA;
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TNR1_RAT
P22934;
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Gaps 10;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                  49 yahpknnsicctkchkgtylvsdcpspggetvcevcdkgtftasgnhvrgclscktcrke 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 L-QYVKQECNRTHNRVCECK--E-GRYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 mfgveispckadmdtvcgckkngfgrylsethfgcvdcspcfng-tvtipckekgntvcn 167
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-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- FTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

-1- FTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

PIR; JN0006; JN0006

PIR; AGOSO4; AGOSO4.

PROSITE: PSO0017; DEATH_DOMAIN.

RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEUER J.G., FATEMIE-NAINIE S., WHEELER E.F., BOTHWELL M.;
DEV. BIOL. 137:287-304 (1990).
-!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
-!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                     22; Mismatches 63; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P., SHOOTER E.M., REICHARDI L.F.; NEURON 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                        Length 461;
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4 X THER-CYS.
THER-CYS 1.
THER-CYS 2.
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Pred. No. 7.09e-23;
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82F68B08 CRC32;
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LAST ANNOTATION UPDATE)
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(REL. 16, LAST SEQI
(REL. 32, LAST ANN
                                                                                                                                                                                                                                         50969 MW;
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                                                                                                                                                                                                                                                                                      / Match 7.7%;
Local Similarity 33.8%;
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01-NOV-1990
01-NOV-1995
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P18519;
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DOMAIN
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CARBOHYD
CARBOHYD
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1-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANDVATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- PIM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 87051725.
JOHNSON D., LANHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E BOTHWELL M., CHAO M.;
CELL 47:545-554(1986).
-! FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3, AND NT-4.
SUBUNT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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EUKARYOTA, META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSÓ0652; INFR_NGFR.
PROSITE; PS50017; DEATH_DOMAIN.
RECEPTOR. NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; PHOSPHORYLATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on 7.5%; Score 215; DB 6; Length 416 Similarity 30.4%; Pred. No. 7.20e-22; 45; Conservative 27; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                         C -> Y (IN REF. 2).
T -> K (IN REF. 2).
N -> S (IN REF. 2).
K -> R (IN REF. 2).
4D3F086A CRC32;
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DEATH DOMAIN.
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C -> Y (IN REF
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PIR; A25218; GQHUN.
HSSP; P19438; ITNR.
MIM; 162010; --
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P08138;
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-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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TNFR-CYS 3.
TNFR-CYS 4.
SER/THR-RICH.
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Best Local Similarity 33.3%;
Matches 43; Conservative
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                                                                          PHOSPHORYLATION; SIGNAL
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                                                                                                                                                                                                                                                                                                    20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHTSDECLYCSPVCKELQYVKQECNR 78
                                                                                                                                                                                                                                                                    5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1988 (REL. 07, CREATED)
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-LIVER;
MEDLINE: 93077038.
MEDLINE: W. ITMMULSPT., ALLIKMETS R., SAARMA M., PERSSON H.;
GENE 121:247-254(1992).
-!- FÜNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
-!- SÜBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RADEKD M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M., NATURE 325:593-597(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOND FORMATION.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PIM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARKOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                 Score 213; DB 6; Length 427;
Pred. No. 1.81e-21;
19; Mismatches 60; Indels
                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                           DEATH DOMAIN.
           RECEPTOR
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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ilarity 34.9%;
Conservative
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Local Similarity
nes 45; Conserv
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427 AA;
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MEDLINE; 87115859.
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                  DOMAIN
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P07174;
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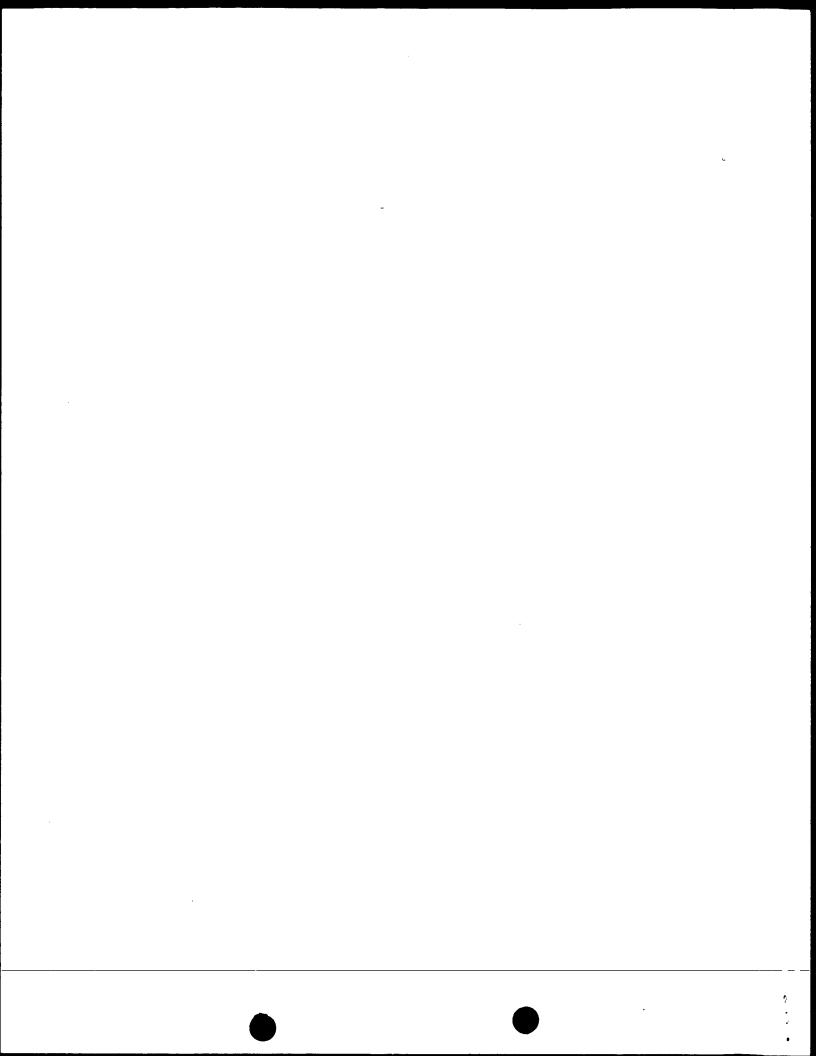
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103 addavcrcaygyyqdeetghceacsvcevgsglvfscqdkqntvceecpegtysdeanhv 162
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MEDLINE; 96226401.
YOO J., STONE R.T., BEATTIE C.W.;
DNA CELL BIOL, 15:277-224(1996).
-!- FUNCTION: RECEPPOR FOR A CYTOKINE LICAND KNOWN AS FASL. MEDIATES
CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
APO-1 ANTIGEN) (CD95).
API OR FAS.
BOS TAGNUS (BOVINE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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د.
EMBL; X05137; G56756; --
EMBL; X61269; -; NOT_ANNOTATED_CDS.
PIR; A26431; A26431.
HSSP: p19438; 1TNN.
PROSTTE: PS00652; TUNR NGFR.
PROSITE; PS50017; DEATH_DOMAIN.
RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 207; DB 6; Length 425;
Pred. No. 2.85e-20;
21; Mismatches 60; Indels
                                                                                                                                                                                                                                                             NGF RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 X INFR-CYS.
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CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC --- SUBCELLULAR T-CELLS, OR BOTH (BY SIMILARITY).
CC --- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC --- SIMILARITY: CONTAINS A LA-NGFK-TWFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; U34794; G1262193; --
FT SIGNAL.
FT SIGNAL.
FT CHAIN 17 323 FAST RECEPTOR.
FT CHAIN 17 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 188 POTENTIAL.
FT DOMAIN 45 163 32 TYRR-CYS.
FT REPEAT 81 124 TYRR-CYS.
FT REPEAT 81 124 TYRR-CYS.
FT REPEAT 81 124 TYRR-CYS.
FT REPEAT 81 124 TYRR-CYS.
FT DOMAIN 222 302
FT DOMAIN 522 302
FT DOMAIN 523 AA; 36445 MW; DA5A2A59 CRC32;
ALCOR SIMILARITY 35.7%; Pred No. 1.51e-16;
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ALCOR SIMILARITY 35.7%; PRED NO. 1.51e-16;
ALCOR SIMIL
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Search completed: Tue Dec 2.14:48:14 1997 Job time: 71 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Dec 3 10:07:14 1997; MasPar time 2.12 Seconds 86.963 Million cell updates/sec Run on:

not generated ular output

(1-15) from US08915004.pep 113 >US-08-915-004-7 Score: Description: Perfect Score Title:

1 ETFPPKYLHYDEETS 15 Sequence:

Scoring table:

Minimum Match 08 Post-processing:

101610 segs, 12294212 residues

Searched:

Listing first 45 summaries

a-geneseq28 Database:

iparil 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21

Mean 19.020; Variance 64.466; scale 0.295 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

tecclastogenesis in 6.54e-0 tated OCIF, OCIF-CP 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tecclastogenesis in 6.54e-0 teated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CB 6.54e-0 tated OCIF, OCIF-CB 6.54e-0 tated OCIF, OCIF-CB 6.54e-0 tated OCIF, OCIF-CB 6.54e-0 tated OCIF, OCIF-CB 6.54e-0 tated OCIF, OCIF-CB 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0 tated OCIF, OCIF-CC 6.54e-0	sult No.	Score	% Query Match	Length	DB	ΩI	Description	Pred. No
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LT 2 899951 standard; Protein; 84 AA. R99951; 23-APR-1997 (first entry)

RESULT

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6.54e-05 6.54e-05 6.54e-05 6.54e-05 6.54e-05 6.54e-05 3.90e-01 1.16e-02 1.16e-02 1.16e-02 1.16e-02 1.16e-02 1.17e-02 1.17e-02 1.77e-02 1.77e-02 1.77e-02 1.77e-02 2.19e-02 2.19e-02 2.19e-02
Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C3 Full length osteolas Bacillus thuringiensi 67-kD protein toxin. Platelet adhesion inh Thermostable beta-gal SDS-resistant hyperth Thermostable beta-gal SDS-resistant hyperth Thermostable beta-gal Bettle patched protein Rat allograft inflamm P.denitrificans COB D Chondrolitnase Ac. Acerypolyamine amido Human ara Kb beta-gal Osteoinductive retrov Rass T1. Malolactic enzyme fro Feline Immunodeficien FIY DUTCH19X1 envelop
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ALIGNMENTS

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DNA conciding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 2: page 67: 183pp; Japanese.

Claim 2: page 67: 183pp; Japanese.

The sequences given in R99921-23 and R99926 represent fragments of the osteoclastogenesis inhibitory factor (OCIF) of the invention.

The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                      22-ApR-1997 (first entry)
Osteoclastogenesis inhibitory factor N-terminal fragment.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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0
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels
                                                                                                                                                                  29-Aug-1996.
20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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R99926 standard; peptide; 15 AA.
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Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                    Homo sapiens.
WO9626217-A1.
                                                                                                                osteoporosis
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Matches
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                                                                                                                                                                                                                                                                                             osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-OFSt in which amno acids 62-380 of the mature OCIF protein are replaced by Leu-Val. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is affect 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutațed OCIF, OCIF-CPst.
Osteșclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1997 (first entry)
Mutated ocif, OciF-OCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoclastogenesis inhibitory factor (OCIF) of the invention. This
                                                                                                                                                                                                                                               DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 89; Page 131; 183pp; Japanese.

This sequence represents a mutated version of the full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 77; Page 125; 183pp; Japanese.
This sequence represents a mutated version of the full length
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                                                                                                                                                                                                 Morinaga T
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 20; Length 84;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels
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21-JUL-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW BRAND MILK PROD CO LTD.
GOCTO | M. Higashio K. Kobayashi F. Mochizuki S.
Nakagawa N. Shima N. Tsuda E. Ueda M. Yano K.
N-PSDB; T33181.
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Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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20 FEB-1995; JP-054977.
21-JUL-1995; JP-207508
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                    Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                          Protein 22..84 //note "Mature OCIF-CPst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein 22.106 /note "Mature OCIF-CCR3"
                                                                             "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 etfppkylhydeets 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETFPPKYLHYDEETS 15
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                                                                                                                                          20-FEB-1996; J00374
                            osteoporosis.
                                                                                                                 WO9626217-A1.
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                                        Synthetic.
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sequence represents OCIF-CCR3 in which amino acids 86-380 of the mature OCIF protein are deleted. The OCIF of the invention mature OCIF protein are deleted. The OCIF of the invention and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. and of is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 74; Page 124; ISBAP; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CCR4 in which amino acids 123:380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption and therefore in the control of sorders of bone resorption, e.g.
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Yasuda H;
                                                                                                                                                                                                                                                                                                                               Score 113; DB 20; Length 106;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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Pred. No. 6.54e-05;
...matches 0; Indels
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29-AUG-1996.
20-FEB-1995; JP-054977.
20-FEB-1995; JP-054977.
21-JUL-1995; JF-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashl F, Mochizuki S, Mc NWPI: 96-402320/40.
NPRSH C AL02320/40.
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22-APR-1997 (first entry)
Osteoclastogenesis inhibitory factor 5.
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R99946 standard; Protein; 143 AA.
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                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
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                                                                                                                                                                                                                                            osteoporosis
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osteoporosis.
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This sequence represents full length osteoclastogenesis inhibitory factor (OCIF) 4. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under norreducing conditions and 120 kD under norreducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 26; page 76-77; 183pp; Japaneses.

This sequence represents full length osteoclastogenesis inhibitory factor (OCIF) 5. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducting conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 5 deg.C. and is lost after 10 mins at 90 deg.C. or useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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      Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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3 9-A07-1996.

20-FEB-1995; JD-054977.

PR 20-FEB-1995; JP-207508.

21-JUL-1995; JP-207508.

PA (SNOW) Higashio K, Kobayashi F, Mochizuki S, Morinaga T; Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; I Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; I Goto M, Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Goto M, I Shima N, Tsuda E, Ucda M, Yano K, Yasuda H; I Shima N, Yano M, Yano K, Yasuda H; I Goto M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yano M, Yan
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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21-JUL-1995; JP-054977.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
(SCOR M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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les 15; Conservation
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n 22.154
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                                                                                                                                                                                Protein 22..145 /note= "Mature OCIF 5"
                                                                                                                            Peptide 1..21
/note= "Signal peptide"
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                                                                         Homo sapiens.
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                                                osteoporosis
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Matches
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This encoding osteoclastogenesis inhibitory factor protein - useful DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 86: Page 130-131; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This concerns the protein are deleted. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is conditions and 120 kD under non-reducing conditions. The protein is a diest 10 may at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and prevention of disorders of bone
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Mutated OCIF, OCIF-CDD1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Mutated OCIF, OCIF-CBsp.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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20-FEB-1995; J00374.
20-FEB-1995; JP-054977.
21-UTL-1995; JP-07508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; NPPI; 96-402320/40.
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useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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100.0%; Score 113; DB 20; Length 187;
Best Local Similarity 100.0%; Pred. No. 6.54e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                       Length 154;
                                                                                                                                                                                                                  Indels
                                                                                                                                          Score 113; DB 20; Le
Pred. No. 6.54e-05;
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187 AA;
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                        15; Conservative
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/note- "Mature OCIF-CBsp"
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                                                                                                                                                                                                                                                                                                                                                1 ETFPPKYLHYDEETS 15
                                                                                                    154 AA;
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 71; Page 123; Baspp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents ourselved in which amino acids 177-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore osteoporosis.
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Na Pouch; 1931.4.

No A encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis

Claim (8h Page 121.12; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CDD2 in which amino acids 252-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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20-FEB-1995; JP-054977.
21-JUJ-1995; JP-207500.
CSNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
Nakagawa N, Shina N, Tsuda E, Ueda M, Yano K, Yasuda H;
N-PSDB; T33174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 113; DB 20; Length 197;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels C
                                                                                     20-FEB-1996; J00374.
21-FEB-1996; JP-054977.
21-JUL-1995; JP-054977.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOto |M, Higashio K, Kobayashi F, Mochizuki S,
Nakadawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33175.
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Best Local Similarity 100.0%;
Matches 15; Conservative
           /notein
/note "Mature OCIF-CDDI"
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Mutated OCIF, OCIF-CDD2.
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"Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide 1..21
/note= "Signal peptide"
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                                                  WO9626217-A1.
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                                                                      29-AUG-1996.
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The properties of the control, esp. treatment of osteoporosis.

To bone resorption control, esp. treatment of osteoporosis.

Claim 83, Page 128-129; 183pp; Japanese.

Control osteoclastogenesis inhibitory factor (OCIF) of the full length of sequence represents a mutated version of the full length of costeoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CSph in which amino acids 298-380 of the mature ocif protein are replaced by Ser-Leu-Asp. These changes are caused by the introduction of a restriction site in the DNA encoding this protein.

The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                          23-APR-1997 (first entry)
Mutated OCIF, OCIF-CSph.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteopozosis.
in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                      Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0; Gaps
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Mutated OCIF, OCIF-DDD1.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
                                                                         Score 113; DB 20; Length 272;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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R99949 standard; Protein; 321 AA.
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                                                                      Match 100.0%;
Local Similarity 100.0%;
les 15; Conservative
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                                                                                                                                        22 etfppkylhydeets 36
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                                    272 AA;
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                     osteoporosis
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 59; Page 115-116; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD2 in which amino acids 253-326 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto
                                                                                                                                                                                                                                                      National Marketing osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoprorosis claim 56; Page 113-114; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DDD1 in which amino acids 178-25 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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Yasuda H;
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
                                                                                                        20-FEB-1996; J00374.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-054977.
SNOW SAND RAND MIK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
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20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
Protein 22..326
/note="Mature OCIF-DDD1"
Misc_difference 198..199
Misc_difference 198..199
Chote="Positition of deletion, delta 178-252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Positition of deletion, delta 253-326"
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/note= "Signal peptide"
Protein 22..327
/note= "Mature CCIF-DDD2"
Misc_difference 273..274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 AA;
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                                                                         WO9626217-A1.
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                                                                                            29-AUG-1996
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Na Fouch 1921/9.

Na Fouch 1921/9.

For bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for for bone respectively. It is the specific of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-CC in which amino acids 331-380 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 50 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-Apr-1997 (first entry)
Mutated OCIF, OCIF-DCR2.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
                                                                                                                                                                                                                                                                                                                      Mutated OCIF, OCIF-CC.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
                                                                                                                    Score 113; DB 20; Length 327;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUC-1996.
20-FEB-1995; JP-054977.
21-UTL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
NAKABAWA N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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R99937 standard; Protein; 359 AA.
                                                                                                                                                                                                                                                                         T 13
R99943 standard; Protein; 351 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0%;
Matches 15; Conservarino
                                                                                                                          Query Match
Best Local Similarity 100.0%;
                                                                                                                      100.0%;
                                                                                                                                                         15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
/note= "Signal peptide"
Protein 22.351
/note= "Mature OCIF-CC"
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                                                                                        327 AA;
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Key
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ID R9
AC R5
DT 21
DE M1
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KW O!
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osteoporosis
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                                                                                                                                                                                                NNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for a bone resorption control, esp. treatment of osteoporosis.

This sequence represents a mutated version of the full length osteopclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR2 in which amino acids 43-84 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kB under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of sorders of bone resorption, e.g.
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Mutated OCIF, OCIF-DCR4
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim[53; Page 111-113; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR4 in which amino acids 123-164 of the mature OCIF protein are deleted. The OCIF of the invention
                                                                                                                                                                                                                                                                                                                                                                                                         Score 113; DB 20; Length 359;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0;
                                                                                                                                                         Morinaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morinaga T;
Yasuda H;
                                                                                                20-FEB-1996; JO0374.
20-FEB-1995; JP-05497.
21-JÜL-1995; JP-207508.
(SNOW SNOW BRAND MILK PROD CO LTD.
GCto | M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-Aug-1996.
20-FEB-1995. JO0374.
20-FEB-1995. JP-054977.
21-JUL-1995. JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
Goto M. Higashio K, Kobayashi F, Mochizuki S,
Nakagwa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB: T33169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein 22.359
/note= "Mature OCIF-DCR4"
Misc_difference 143..144
/note= "Positition of deletion, delta 123-164"
                                              Misc_difference 63..64
/note= "Position of deletion, delta 43-84"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R99939 standard; Protein; 359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.0%;
les | 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                          rotein 22..359
 "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide 1..21
/note= "Signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                   359 AA;
                                                                        WO9626217-A1.
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                                                                                      29-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                         Protein
 Peptide
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Matches
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ID R9
AC R9
DT 23
DE Mu
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has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers on reducing and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis. Claim SO, Page 109-111; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-DCR3 in which amino acids 85-122 of the mature OCIF protein are deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption and therefore in the control of sorders of bone resorption, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR3.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                    Score 113; DB 20; Length 359;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels C
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21-PEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW SNOW BRAND MILK PROD CO LTD.
GCto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; Ţ33168.
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22-APR-1997 (first entry)
Mature osteoclastogenesis inhibitory factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc_difference 105..106
/note= "Position of deletion, delta 85-122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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R99938 standard; Protein; 360 AA.
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                                                                                                                                                                                                                                                                          100.0%;
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ses 15; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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/note= "Signal peptide"
Protein 22..360
/note= "Mature OCIF-DOR3"
                                                                                                                                                                                                                                                                                                                                                                                             22 etfppkylhydeets 36
                                                                                                                                                                                                                                                                                                                                                                                                                               1 ETFPPKYLHYDEETS 15
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                                                                                                                                                                                                               359 AA;
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New human tumour necrosis factor receptor - used to develop prods. For treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation claim. The rejection cytotoxicity or inflammation claim. The receptor binds to TNE, and in particular, TNF-beta.

The receptor may be used for screening for antagonists and agonists of the receptor and for ligands for the receptor. Such agonists may be used to inhibit the growth of tumours, to stimulate cellular differentiation, to mediate the immune response and anti-viral response, to regulate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat autoimmune diseases, inflammation, septic shock, to inhibit graft. Versus-host reactions, and to prevent apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                            DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis This sequence represents the mature osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1997 (first entry)
Human tumour necrosis factor receptor.
Human tumour necrosis factor TNF; receptor.
Tumour necrosis facor; TNF; receptor; TNF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
septic shock; graft-versus-host; apoptosis.
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                                                                                                                                                                        Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 113; DB 20; Length 380;
Pred. No. 6.54e-05;
0; Mismatches 0; Indels
                                                                                    20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T36685.
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R99357 standard; Protein; 390 AA.
R99357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-1996.
15-MAR-1995; U03216.
15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
(HUMA-) HUMAN GENOME SCI INC.
Fleischmann RD, Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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WO9628546-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 AA;
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                    osteoporosis.
                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis
                                                                          29-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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DB 20; Length 390;

100.0%; Score 113;

Query Match

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National State of the protein of the full length of the modified of the modern of the modern of the modern of the modern of the full length of the sequence represents a mutated version of the full length of the sequence represents a mutated version of the full length of the sequence represents a mutated version of the invention. This sequence represents the sequence (OCIF) of the invention. This sequence represents ocir-Cabat in which din 371 is substituted by the new order of the mature ocif protein are deleted. These changes are caused by the introduction of a restriction site in the DNA encoding this protein. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
                               Indels
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
31-JUL-1995; JP-207508.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Makagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; T33178.
   Pred. No. 6.54e-05;
0; Mismatches 0;
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R99942 standard; Protein; 399 AA.
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R99948 standard; Protein; 393 AA.
R99948;
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Matches 15; Conservative
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/note= "Mature OCIF-CBst"
Misc_difference 392
                               15; Conservative
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Protein 22.399
/note= "Mature OCIF-CL"
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                                                                                    1 ETFPPKYLHYDEETS 15
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w09626217-A1.
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                                                                                                                                                                                                                                                                             for bone resorption control, esp. treatment of osteoporosis
Claim 62: Page 117-119; 183pp; Japanese.
This sequence represents a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence represents OCIF-CL in which amino acids 379-380 of the
mature OCIF protein are deleted. The OCIF of the invention
has a molecular weight by SDS-PAGE of 60 bunder reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins
at 70 deg.C. OCIF is useful in the control of bone resorption and thatefore
in the treatment and prevention of disorders of bone resorption, e.g.
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To bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for bone resorption control, esp. treatment of osteoporosis for bone resorption control, 183pp; Japanese.

This sequence represents a mutated version of the full length osteograstogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C21S in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has all molecular weight by SDS-PAGE of 60 kD under reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C, OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Osteoplastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
Goto M. Higashio K, Kobayashi F, Mochizuki S, Makagawa N, Shima N, Tsuda E, Ueda M, Yano K, N-PSDB; T33163.
                                                                                                                                                        Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI: 196-402320/40.
N-PSDB; T33172.
                                              20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995, JP-207508.
SNOW BRAND MIK PROD CO LTD.
GOCO |M, Higashio K, Kobayashi F, M
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Matches 15; Conservative
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/note= "Mature OCIF-C21s"
Misc_difference 277
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/note= "Signal peptide"
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Mutated OCIF, OCIF-C23S.
Osteoolastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
21-JUL 1995; JP-207508.
GOTO M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T; Nakaqawa N, Shina N, Tsuda E, Ueda M, Yano K, Yasuda H; N-PSDB; T33162.
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
                                              Length 401;
                                         Score 113; DB 20; Length 401
Pred. No. 6.54e-05;
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R99932 standard; Protein; 401 AA.
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nes 15; Conservative
                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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22-APR-1997 (first entry)
Mutated OCIF, OCIF-C20S.
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'note= "Mature OCIF-C20S"
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                                                                                                                                1 ETFPPKYLHYDEETS 15
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             401 AA;
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WO9626217-A1.
29-AUG-1996.
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osteoporosis
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 41. Page 103-105; 183pp; Japanese.

This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C23S in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of some resorption and therefore in the control of some resorption of cisocders of bone resorption, e.g.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C22S in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto
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Yasuda H;
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
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29-AUG-1996, 200374.
20-FEB-1996; JP-054977.
R 20-FEB-1995; JP-207508.
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
T GOLD M, Higashio K, Kobayashi F, Mochizuki S, Mor Gold M, Shima N, Tsuda E, Ueda M, Yano K, Ya
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
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22..401
/note= "Mature OCIF-C23S"
Misc_difference 400
/label= C23S
W09655
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Best Local Similarity 100.0%;
Matches 15; Conservative
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22-APR-1997 (first entry)
Mutated OCIF, OCIF-C22S.
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/note= "Mature OCIF-C228"
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/label= C22s
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WPI; 96-402320/40.
N-PSDB; T33164.
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This sequence represents a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence represents OCIF-C19S in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of e.g.
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cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.c. or 30 mins at 56 deg.c, and is lost after 10 mins at 90 deg.c. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Full length osteoclastogenesis inhibitory factor.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-APR-1997 (first entry)
Mutated OCIF, OCIF-C19S.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis.
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Yasuda H;
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels (
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0
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20-FEB-1996; JO0374.
20-FEB-1996; JO05497.
21-UFL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S,
Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K,
N-PSDB; T33161.
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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/note= "Mature OCIF-C195"
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/note= "Signal peptide"
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W09626217-A1.
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W0962617-A1.

29-A¢G-1996.

29-A¢G-1996.

29-A¢G-1996.

20-EEB-1995; JP-054977.

PR 21-J¢L-1995; JP-054977.

PR 21-J¢L-1995; JP-054977.

PR 21-J¢L-1995; JP-054977.

PR 21-J¢L-1995; JP-207508.

PR 21-J¢L-1995; JP-207508.

PR (Goto) M. Hidashio M. Kobayashi F. Mochizuki S. Morinaga T;

NARagawa N. Shima N. Tsuda E. Ueda M. Yano K. Yasuda H;

NF1: |96-402320/40.

NF1: |96-402320/40.

PT (Goto) M. Hidashio Steoclastogenesis inhibitory factor protein - useful

For bone resorption control, esp. treatment of osteoporosis

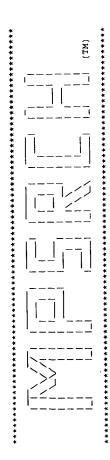
Disclosure; Page 64-66. 183pp; Japanese Disclosure; Page 64-66. 183pp; Japanese Disclosure; Page 64-66. 183pp; Japanese Disclosure; Page 64-66. 183pp; Japanese Costeoporosis

This sequence represents the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by factor (OCIF) of the invention and adorbed onto cation-exchangers

CSDS-pAGE of 60 Wunder reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers

CSDS-pAGE of 60 Wunder reducing sea of deg.C or correction is a stater 10 mins at 70 deg.C or correction is a stater 10 mins at 70 deg.C or correction of the factor of the resorption, e.g.
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Pred. No. 6.54e-05;
0; Mismatches 0; Indels 0;
                    Location/Qualifiers
                                                                                Protein 22..401
/note= "Mature OCIF, claim 6"
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Best Local Similarity 100.0%;
Matches 15; Conservative
                                     Peptide 1..21
/note= "Signal peptide"
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  Homo sapiens.
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Search completed: Wed Dec 3 10:07:20 1997 Job time : 6 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Tue Dec 2 14:52:31 1997; MasPar time 2.86 Seconds 151.367 Million cell updates/sec

pular output not generated.

Run on:

>US-08-915-004-7 (1-15) from US08915004.pep 113 Description: Perfect Score: ttle:

1 ETFPPKYLHYDEETS 15 Sequence:

PAM 150 Gap 15 Scoring table:

91006 seqs, 28888923 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev pir51 Database:

Mean 26.254; Variance 43.975; scale 0.597 Statistics:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	3.59e-01	7.73e-01	2.38e+00	2.38e+00	4.95e+00	4.95e+00	1.01e+01	1.01e+01	2.05e+01			2.05e+01	2.05e+01	2.05e+01	2.89e+01	2.89e+01		2.89e+01	2.89e+01	2.89e+01	2.89e+01
Description	probable membrane pr	histidine decarboxyl	beta-fructofuranosid	beta-fructofuranosid	MHC class I protein	cytochrome-c oxidase	hypothetical protein	72K crystal protein	hypothetical protein	hypothetical protein		cytochrome-c oxidase	hypothetical protein	probable membrane pr	farnesyl-pyrophospha	ribulose-bisphosphat	malate oxireductase	acetylcholinesterase	acetylcholinesterase	probable amino acid	arylphorin precursor
ΙΩ	S53409	S49218	S61503	JQ0991	I50036	526034	S67612	A43647	S01180	S07880	H37386	S26022	S40822	S55151	A35726	JC2307	544330	ACRYE	A38868	S54032	JQ1045
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Length 1932;

Query Match 59.3%; Score 67; DB 12; Length 1932 Best Local Similarity 46.2%; Pred. No. 3.59e-01; Matches 6; Conservative 4; Mismatches 3; Indels

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RESULT

ENTRY

ORGANISM

DATE

849218 #type complete
histidine decarboxylase (EC 4.1.1.22) - Vibrio anguillarum
histidane Vibrio anguillarum
16-reb-1995 #sequence_revision 12-May-1995 #text_change
22-Nov-1996

Tolmasky, M.E.; Actis, L.A.; Crosa, J.H.

S60898; S49218 S60898

#authors ACCESSIONS REFERENCE

4 47.8 154 3 4 47.8 155 7 4 47.8 169 12 4 47.8 165 19 14 47.8 165 19 14 47.8 165 19 14 47.8 165 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.9 19 18 46.0 15	egg-lysin precursor 4.06e+01 hypothetical protein 4.06e+01 hypothetical protein 4.06e+01 ribulose-bisphosphat 4.06e+01 outer membrane prote 4.06e+01 probable membrane pr 4.06e+01 chromogranin-B - rat 5.68e+01 A52R protein - vac:1 5.68e+01 lipA protein - vac:1 5.68e+01 salF15R protein - va 5.68e+01 lipA protein - vac:1 5.68e+01 beta-galactosidase (5.68e+01 beta-galactosidase (5.68e+01 cytochrome P450 lA 5.68e+01 chondroitin sulfate 5.68e+01 chondroitin sulfate 5.68e+01 chondroitin sulfate 5.68e+01 allograf inflammato 7.92e+01 ribosomal protein 7.92e+01 ribosomal protein 7.92e+01 ribosomal protein 7.92e+01 ribosomal protein 7.92e+01 bypothetical protein 7.92e+01 bypothetical protein 7.92e+01 bypothetical protein 7.92e+01 bypothetical protein 7.92e+01	The complete Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 Transmembrane #status predicted #label TM2 #molecular-weight 221561 #checksum 5013
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                               SUMMARY
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Plant J. (1993) 4:545-554
Molecular characterization of the gene for carrot cell wall
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Plant Cell (1990) 2:1107-1119
cDNA cloning of carrot extracellular beta-fructosidase and its expression in response to wounding and bacterial
                                                                                                                                                               carbon-carbon lyase; carboxy-lyase; pyridoxal phosphate
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                                                                                                                                                                                                  #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-fructofuranosidase (EC 3.2.1.26) - carrot
#formal_name Daucus carota #common_name carrot
27-Oct-1996 #sequence_revision 27-Oct-1996 #text_change
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             A histidine decarboxylase gene encoded by the Vibrio anguillarum plasmid pJM1 is essential for virulence: histamine is a precursor in the biosynthesis of
                                                                                                                                                                                                                              #length 386 #molecular-weight 44260 #checksum 4338
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##cross-references EMEL:X69321
XX #length 592 #molecular-weight 66871 #checksum 4674
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Pred. No. 2.38e+00;
0; Mismatches 5; Indels
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Pred. No. 7.73e-01;
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##residues 1-592 ##label STU
##cross-references GB:M58362
FPICATION #superfamily beta-fructofuranosidase
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   Mol. Microbiol. (1995) 15:87-95
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Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.R.
Genetics (1992) 130:471-498
The mitochondrial genomes of two nematodes, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grossberger, D.; Parham, P.
Immunogenetics (1992) 36:166-174
Reptilian class I major histocompatibility complex genes
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                              MHC class I protein - axolotl (fragment)
#formal_name Ambystoma mexicanum #common_name axolotl
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
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glycosidase; hydrolase
#length 592 #molecular-weight 66813 #checksum 3928
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#cross-references MUID:92307752
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##residues 1-37 ##label GRO
##cross-references GB:M81089; NID:g210935; CDS_PID:g555414
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                                                                                Length 592;
                                                                      Score 62; July,
Pred. No. 2.38e+00;
"...marrhes 5; Indels
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Pred. No. 4.95e+00;
1; Mismatches 1; Indels
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                                                                      Ouery Match
Best Local Similarity 61.5%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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J. Bacteriol. (1988) 170:4732-4738
Molecular characterization of a gene encoding a 72-kilodalton
mosquito-toxic crystal protein from Bacillus thuringlensis
subsp. israelensis.
                                                                                                                                                                                                                                                    #domain cytochrome-c oxidase chain I homology *label COI
#length 525 #molecular-weight 58463 #checksum 9978
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                                                                                                                                       *superfamily cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology copper binding; electron transfer; heme; membrane-associated
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03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
               the authors translated the initiation codon ATT for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical, protein D2476
#formal_name Saccharomyces cerevisiae
12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change
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Wambutt, R.; Wedler, H.; Wedler, E.; Scharfe, M.
submitted to the Protein Sequence Database, July 1996
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                                                                                                                                                                                                  complex; mitochondrion; oxidative phosphorylation;
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72K crystal protein - Bacillus thuringiensis subsp.
israelensis
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hypothetical protein YDL076c - yeast (Saccharomyces
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Pred. No. 1.01e+01;
4; Mismatches 2; Indels
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EMBL: X54252
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A43647; A32256
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hypothetical protein 1 - Methanobacterium thermoautotrophicum
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                                                           #authors Adams, L.F.; Visick, J.E.; Whiteley, H.R.
#journal J. Bacteriol. (1989) 71:521-530
#title A 20.kilodalton protein is required for efficient production of the Bacillus thuringiensis subsp. israelensis 7. kilodalton crystal protein in Escherichia coll.
#cross-references MUID:89123065
#accession A3226
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Mucleic Acids Res. (1988) 16:4053-4067
Analysis of the entire nucleotide sequence of the cryptic plasmid of Chlamydia trachomatis serovar Ll. Evidence for
                                                                                                                                                                                                                          preliminary; not compared with conceptual translation
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hypothetical protein N-1 - Chlamydia trachomatis plasmid
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07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
18-Jun-1993
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30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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#length 203 #molecular-weight 23076 #checksum 8385
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#length 643 #molecular-weight 72348 #checksum 6237
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Nucleic Acids Res. (1990) 18:363
Complete nucleotide sequence of plasmid pME2001 of
Methanobacterium thermoautotrophicum (Marburg).
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                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 10; Length 643
Pred. No. 1.01e+01;
2; Mismatches 1; Indels
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#cross-references MUID:88233998
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##residues 566-643 ##label ADA
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##residues 1-643 ##label DON
##cross-references GB:M31737
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Local Similarity 41.7%;
hes 5; Conservative
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Best Local Similarity 70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Comanducci, M.; Ricci, S.; Ratti, G.
#journal Mol. Microbiol. (1988) 2:531-538
#title The structure of a plasmid of Chlamydia trachomatis believed
to be required for growth within mammalian cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Comanducci, M.; Ricci, S.; Cevenini, R.; Ratti, G. Plasmid (1990) 23:149-154
Diversity of the Chlamydia trachomatis common plasmid in biovars with different pathogenicity.
                                                                                                                                                              Gaps
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17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
01-Dec-1995
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Pred. No. 2.05e+01;
5; Mismatches 2; Indels
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NCE | S31169
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##residues
1-330 ##label COMI
##cross-references GB:J03321
SNCE | $01920
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##residues 1-330 ##label COM2
##cross-references EMBL:X07547
                1-273 ##label BOK
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##experimental_source plasmid pcT
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S26022 #type complete cytochrome-c oxidase (EC 1.9.3.1) chain I - pig roundworm

\$26022

RESULT

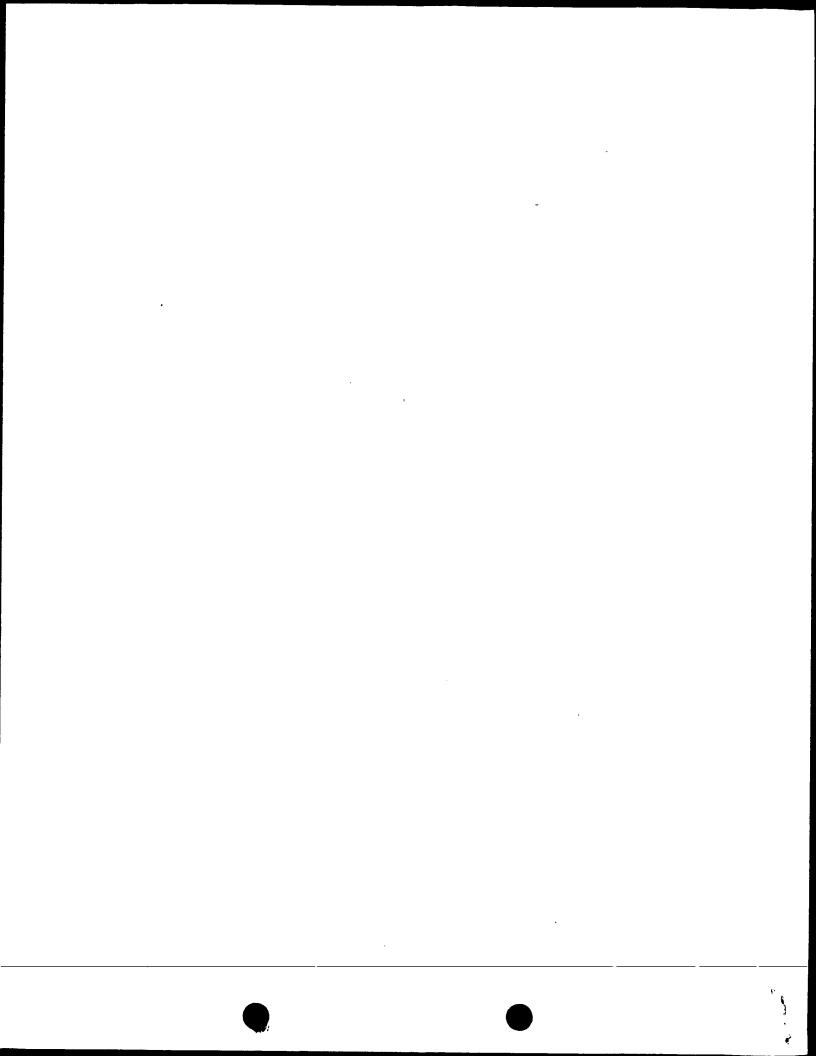
TITLE

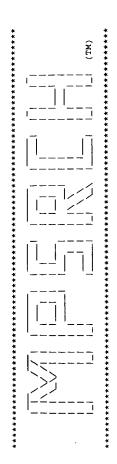
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Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R. Nucled. Acids Res. (1993) 21:3391-3398
Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.
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##note to the EMBL bata
                                                                                                                                                                                                                                                                                             two nematodes, Caenorhabditis
                                                                                                                                                                                                Okimoto, R.; Macfarlane, J.L.; Clary, D.O.; Wolstenholme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okimoto, R.; Macfarlane, J.L.; Wolstenholme, D.R. Nucleic Acids Res. (1990) 18:6113-6118 Evidence for the frequent use of TTG as the translation initiation codon of mitochondrial protein genes in the nematodes, Ascaris suum and Caenorhabditis elegans.
                        #formal_name mitochondrion Ascaris suum #common_name pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the authors translated the initiation codon ATT for residue 1 as 1le
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##note the authors translated the initiation codon ATT for
residue 1 as 11e
                                                   roundWorm
12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change
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hypothetical protein f678 - Escherichia coli
#formal_name Escherichia coli
19-May-1994 #sequence_revision 01-Sep-1995 #text_change
01.Sep-1995
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#length 525 #molecular-weight 58529 #checksum 1290
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translation not shown
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Best Local Similarity 50.0%; Pred. No. 2.05e+01;
Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                         #journal Genetics (1992) 130:471-498
#title The mitochondrial genomes of
the medians and Ascaris suum.
#cross-references MUID:92201635
#accession $286022
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##residues 1-525 ##label OKI
##cross-references EMBL:X54253
mitochondrion (SGC4)
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##residues 1-25 ##label OK2
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                                                                ACCESSIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mallet, L.; Bussereau, F.; Jacquet, M.
Yeast (1995) 11:1195-1209
A 43.5 kb segment of yeast chromosome XIV, which contains
MFA2, MEP2, CAP/SRV2, NAM9, FKBI/FPRI/RBP1, MOM22 and CP11,
predicts an adenosine deaminase gene and 14 new open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                        hypothetical protein JTA1056; hypothetical protein N1216
                                                                                                                                                                                                                                                  probable membrane protein YNL132w - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                         hypothetical protein N1858
#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain transmembrane #status predicted #label TMM #length 1056 #molecular-weight 119346 #checksum 3315
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mallet, L.; Bussereau, F.; Jacquet, M. submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A35726 #type complete
farnesyl-pyrophosphate synthetase - human
prenyltransferase and farnesyl-diphosphate synthase
dimethylallyltranstransferase (EC 2.5.1.1);
               #length 678 #molecular-weight 77248 #checksum 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the nucleotide sequence was submitted to the Library, November 1994
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                                                                                                                                                                                                                                                                                                                                                                                                  Mallet, L.; Bussereau, F.; Jacquet, M. submitted to the EMBL Data Library, November 1994 A 43.5 kb fragment of the chromosome XIV. 555151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 12; Length 1056;
Pred. No. 2.05e+01;
0; Mismatches 1; Indels (
                                                 Score 56; DB 9; Length 678; Pred. No. 2.05e+01;
                                                                                         1; Indels
                                                                                         5; Mismatches
Library, October 1993
                                                                                                                                                                                                                                       #type complete
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##residues 1-1056 ##label MAW
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Local Similarity 85.78;
                                                       49.68;
                                                                        Best Local Similarity 40.0%;
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                                                                                           4; Conservative
                                                                                                                                                                                                                                                                             cerevisiae)
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Sheares, B.T.; White, S.S.; Molowa, D.T.; Chan, K.; Ding, V.D.H.; Kroon, P.A.; Bostedor, R.G.; Karkas, J.D. Biochemistry (1989) 28:8129-8135 Cloning, analysis, and bacterial expression of human farnesyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                    Wilkin, D.J.; Kutsunai, S.Y.; Edwards, P.A.
J. Biol. Chem. (1990) 265:4607-4614
Isolation and sequence of the human farnesyl pyrophosphate
synthetase CDNA. Coordinate regulation of the mRNAs for
farnesyl pyrophosphate synthetase,
3-hydroxy-3-methylglutaryl coenzyme A reductase, and
3 hydroxy-3-methylglutaryl coenzyme A synthase by phorbol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
geranyltranstransferase (EC 2.5.1.10)
#formal_name Homo sapiens #common_name man
30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
06-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pyrophosphate synthetase and its regulation in Hep G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 1; Length 353;
Pred. No. 2.89e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
##residues 8-115,'I',117-353 ##label SHE
##cross-references GB:M29863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-353 ##label WIL
##cross-references GB:J05262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##cross-references GDB:128629
                                                                                                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:90170972
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Best Local Similarity 33.3%;
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KEYWORDS
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Dec 2 14:52:04 1997; MasPar time 2.01 Seconds 158.672 Million cell updates/sec Run on:

>US-08-915-004-7 (1-15) from US08915004.pep 113 1 ETFPPRYLHYDEETS 15 plar output not generated.

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

59021 seqs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 Mean 27.188; Variance 37.530; scale 0.724 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	مري	Query	I.ength DR	E C	Ę	Description	Pred. No.
	10000	1133 111		;			,
	62	54.9	592	2	INVA DAUCA	BETA-FRUCTOFURANOSIDA	4.87e-01
7	9	53.1	252	6	TRYI DROME	TRYPSIN IOTA PRECURSO	1.15e+00
m	9	53.1	423	11	YPIA_BACSU	HYPOTHETICAL 48.3 KD	1.15e+00
4	9	53.1	525	7	COX1_CAEEL	CYTOCHROME C OXIDASE	1.15e+00
5	59	52.2	1188	m	DPOL_ADE40	DNA POLYMERASE (EC 2.	1.75e+00
9	58	51.3	643	7	CR72_BACTI	72 KD CRYSTAL PROTEIN	2.65e+00
7	56	49.6	273	1	YP30_METTH	HYPOTHETICAL 30.7 KD	6.01e+00
80	56	49.6	332	4	GP8D_CHLTR	VIRULENCE PROTEIN PGP	6.01e+00
σ	56	49.6	458	œ	RBL2_RHOCA	RIBULOSE BISPHOSPHATE	6.01e+00
10	26	49.6	510	11	YQBA_BACSU	HYPOTHETICAL 58.5 KD	6.01e+00
11	56	49.6	525	7	COX1_ASCSU	CYTOCHROME C OXIDASE	6.01e+00
. 12	56	49.6	678	11	YIHQ_ECOLI	HYPOTHETICAL 77.2 KD	6.01e+00
13	56	49.6	804	ω	RIR1_HSV6U	RIBONUCLEOSIDE-DIPHOS	6.01e+00
14	56	49.6	1056	Ξ	YNN2_YEAST	HYPOTHETICAL 119.3 KD	6.01e+00
15	55	48.7	353	4	FPPS_HUMAN	FARNESYL PYROPHOSPHAT	8.97e+00
16	55	48.7	565	ø	MAOX_SCHPO	MALATE OXIDOREDUCTASE	8.97e+00
17	55	48.7	586	-	ACES_TORCA	ACETYLCHOLINESTERASE	8.97e+00
18	55	48.7	590	П	ACES_TORMA	ACETYLCHOLINESTERASE	8.97e+00
19	55	48.7	604	^	PAP1_YEAST	PUTATIVE AMINO-ACID P	8.97e+00
20	55	48.7	759	Н	ARY1_CALVI	ARYLPHORIN A4 PRECURS	8.97e+00
21	54	47.8	154	٣	ELYS_HALWA	EGG-LYSIN PRECURSOR (1.33e+01
22	54	47.8	154	m	ELYS HALSO	EGG-LYSIN PRECURSOR (1.33e+01

1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01 1.33e+01	800000	j ω ω ω ω ω	2.89e+01 2.89e+01 2.89e+01 2.89e+01
EGG-LYSIN PRECURSOR (EGG-LYSIN PRECURSOR (PUTATIVE TRANSCRIPTIO RIBULOSE BISPHOSPHATE RIBULOSE BISPHOSPHATE RIBULOSE BISPHOSPHATE ROW-REGULATED OUTER SUCROSE SYNTHASE (EC HYPOTHETICAL 117.0 KD	HYPOTHETICAL 130.8 KD PROTEIN A52. CAPGILE POLYSACCHARID PROBABLE 6-PHOSPHO-BE	BETA-GALACTOSIDASE (E BETA-GALACTOSIDASE (E BETA-GALACTOSIDASE (E LEU/VAL/ILE AMINO-ACI HYPOTHETICAL PROTEIN HYPOTHETICAL OXIDORED	PUTATIVE SERINE CARBO HYPOTHETICAL PROTEIN HYPOTHETICAL 92.1 KD BOTULINUM NEUROTOXIN
ELYS_HALRU ELYS_HALCO TFS2_CAEEL RBL2_RHOSH RBL2_RHORU IRGA_VIBCH SUSY_ALNGL	YMV2_CAEEL VA52_VACCC VA52_VACCV LIPA_NEIME GLVG_BACSU	BGAL_SULSH BGAM_SULSO BGAL_SULSO BAP2_YEAST YOO6_MYCGE	YSS2_CAEEL Y241_MYCGE YA73_SCHPO BXE_CLOBO
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ALIGNMENTS

RESULT						
S I	INVA_DAUCA	STAN	STANDARD;	PRT;	592 AA.	
占	01-AUG-1992	(REL.	CREAT	_		
텀	01-AUG-1992	(REL.	23, LAST SEC	LAST SEQUENCE UPDATE)	PDATE	
2 E	OI-FEB-1996 (REL. 33, LAST ANNOIALION OFDAIR BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME	(REL. 3	S, LAST AND DASE, INSOI	UBLE ISC	OFDAIL)	3.2.1.26)
吕吕	(SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE)	HOSPHAT	E HYDROLASI	E) (INVE		
SO	DAUCUS CAROT	CAROTA (CARROT	OT).			
႘	EUKARYOTA; F	LANTA;	PLANTA; EMBRYOPHYTA;		ANGIOSPERMAE; DICOTYLEDONEAE;	ME; APIALES;
႘	UMBELLIFERAE	.:				
RN	[1]				!	
RP		N N.A.		AL SEQUENCE	ACE.	
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XX.	Э	93005650.				
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N.		1	. (0001)011			
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RX	MEDLINE: 940	94035200.				
R.A	\vdash	×	KNUDSEN S.,	STURM A.:		
RL	PLANT J. 4:5	554 (,			
ပ္ပ		I: MAY P		IMPORTANT R	ROLE IN PHLOEM UNLOADING	ING AND IN
ပ္ပ	STRESS F	RESPONSE				
ပ္ပ	-!- CATALYTI	C ACTIV	ITY: HYDRO	LYSIS OF	CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING	NG BETA-D-
ပ္ပ	FRUCTOFU	FRUCTOFURANOSIDE	E RESIDUES	IN BETA	RESIDUES IN BETA-D-FRUCTOFURANOSIDES.	
ပ္ပ	-i- SUBCELLI	JLAR LOC	ATION: ION	ICALLY BO	SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL	. i
ပ္ပ	-:- INDUCTIC	N: IN R	INDUCTION: IN RESPONSE TO	WOUNDIN	TO WOUNDING AND BACTERIAL INFECTION	CTION.
ပ္ပ	-!- SIMILAR	TY: BEL	ONGS TO FA	MILY 32 (SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES	
ပ္ပ		R AT LE	AST THREE	ISOZYMES	THERE ARE AT LEAST THREE ISOZYMES OF BETA-FRUCTOFURANOSIDASE	DSIDASE IN
ပ္ပ	α,	ONE INS		TWO SOL	UBLE.	
DR		M58362; G167551;	••			
DR	EMBL; X69323	x69321; G18324;	4;			
DR	PIR; JQ0991,	100001		1		
DR	U)	00609; G	LYCOSYL_HY	DROL_F32		
X	ASE;	GLYCOSIDASE;		PROTEIN;	GLYCOPROTEIN; CELL WALL; ZIMOGEN;	SIGNAL.
H	SIGNAL	٦;	31	<u>س</u>	(POTENTIAL).	
FT	PROPEP	32	m	OR 40 (P		
FT	CHAIN	4 9		BETA-FRU	OFURANOSIDASE,	INSOLUBLE
H				I SOENZYME.		
ЕŢ	ACT_SITE	74		BY SIMILARITY		
FT	CARBOHYD	170	170	COMPLEX-TYPE	TYPE GLYCAN.	
FF	CARBOHYD	195	195	POTENTIAL.		
FŢ	CARBOHYD	311	311	COMPLEX-TYPE	TYPE GLYCAN.	
БŢ	CARBOHYD	348	348	HIGH-MAN	HIGH-MANNOSE-TYPE GLYCAN.	
FI	CARBOHYD	210	570	POTENTIAL	년.	
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COX1_CAEEL
P24893;
                                                                  SEQUENCE
                                                                                                                           Query Match
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REQUIRED FOR SPECIFICITY (BY SIMILARITY).
; CE103ACF CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAO L, WANG S., HICKEY D.A.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYITC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-|-XAA, LYS-|-XAA.
-!- SÜBCELLULAR LOCATION: EXTRACELLULAR.
-!- SÜBLELULARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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STRAIN=168 / MARBURG;
SOROKIN A.V., AZEVEDO V., ZUMSTEIN E., GALLERON N., EHRLICH S.D.,
SERROR P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
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FLYBAŞE; FBGN0015001; TRY-IOTA.
HYDROĻASE; SERINE PROTEASE; ZYMOGEN; SIGNAL; MULTIGENE FAMILY.
                                                                                                                Score 62; DB 5; Length 592;
Pred. No. 4.87e-01;
                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 252;
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133 R -> W (IN REF. 2).
487 A -> V (IN REF. 2).
66813 MW; D41B4A3C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60; DB 9; LA
Pred. No. 1.15e+00;
3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CP-1996 (REL. 34, CREATED)
01-0CP-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CP-1996 (REL. 34, LAST ANNOTATION UPDATE)
TRYPSIN IOTA PRECURSOR (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 48.3 KD PROTEIN IN QCRA 5'REGION
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           PRT; 252 AA
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                                                                                                                54.9%;
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ilarity 54.5%; Conservative
                                                                                                                                                                      8; Conservative
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     133
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252
68
113
206
                                                                                                                                                                                                                       435 epfdpkwleydae 447
                                                                                                                                                                                                                                                          103 eqfdsrflhyd 113
                                                      592 AA;
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | :::||||
ETFPPKYLHYD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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P54389;
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GENETICS 130:471-498(1992).

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE BNIYME. BLECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT I TO THE BIMETALLIC CENTER FORMED BY HEME AS AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLOLAR LOCATION: INTEGRAL MENBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
-1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE.FAMILY. EMBL. X54252; G515883; --
PIRIS, S26034; S26034.
PROSITE; PS00077; COXI.
OXIDOREDUCTARE: HEME; COPPER; MITOCHONDRION; TRANSMEMBRANE;
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
-!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                        Score 60; DB 11; Length 423; Pred. No. 1.15e+00;
                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A3) (PROBABLE).
IRON (HEME A) (PROBABLE).
MW; FBD63AAD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESPIRATORY CHAIN; INNER MEMBRANE.

METAL 69 69 IRON (HEME A) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                           01-MAR'1992 (REL. 21, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.15e+00;
                                        423 AA; 48321 MW; 708A0553 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 5
DPOL_ADE40
BY 84311;
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DNA POLYMERASE (EC 2.7.7.7).
                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                         525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60;
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58463 MW;
                                                                                           53.1%;
                                                                                                              46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  larity 60.0%;
Conservative
                                                                                                                                        Conservative
SUBTILIST; BG11496; YPIA
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3838
                                                                                                                                                                                 361 qsfeaaylhyred 373
                                                                                                                                                                                                                            1 ETFPPKYLHYDEE 13
                   HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251
297
298
298
383
385
525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 fprkyldypd 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 92201635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 FPPKYLHYDE 12
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4 PPKYLHYDEETS 15
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             CHLAMYDIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMID
                                                                                                                              Query Match
                                                                                                                                                                                                                                        æ
                                                                                                                                                        Matches
                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS THURINGIENSIS (SUBSP. ISRAELENSIS).
PROKARYOTA, FIRMICUTES, ENDOSPORE-FORMING RODS AND COCCI, BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DONOVAN W.P., DANKOCSIK C., GILBERT M.P.;
J. BACTERIOL. 170:4732-4738(1988).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPITHELIAL CELLS OF MOSQUITOS.
-!- TOXIC SEGRENT OF THE PROTEIN IS LOCATED IN THE N-TERMINUS.
-!- DEVELOPMENTAL STAGE: THE CRISTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS PART
                        VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES
                                                                                                                                                                                                                               Gaps
                                                                       DAVISON A.U. TELFORD E.A., WATSON M.S., MCBRIDE K., MAUTNER V.;
DAVISON A.U. TELFORD E.A., WATSON M.S., MCBRIDE K., MAUTNER V.;
J. MOL. BIOL. 234:1308-1316(1993).
-!- CAPALITIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
N PYROPHOSPHATE + DAMA(N).
-!- THIS DNA POLYMERASE REQUIRES A PROTEIN AS A PRIMER.
-!- SIMILARITY: BELONGS TO FAMILY B OF DNA POLYMERASES.
EMBL. 119443; G303975; -.
DNA-DIRECTED DNA POLYMERASE; DNA REPLICATION; DNA-BINDING.
SEQUENCE 1188 AA; 135289 MW; CREE6098 CRC32;
                                                                                                                                                                                                                                                                                                                                                      01-WAY-1991 (REL. 18, CREATED)
01-WAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
01-WAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
72 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 51.3%; Score 58; DB 2; Length 643; Local Similarity 70.0%; Pred. No. 2.65e+00; Pred. 7; Conservative 2; Mismatches 1; Indels pas
                                                                                                                                                                                                    / Match 52.2%; Score 59; DB 3; Length 1188; Local Similarity 60.0%; Pred. No. 1.75e+00; nes 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMID PME2001.
ARCHAEBACTERIA, EURYARCHAEOTA, METHANOBACTERIALES;
METHANOBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 AA; 72348 MW; 0C528C2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
HYPOTHETICAL 30.7 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                               643 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHANOBACTERIUM THERMOAUTOTROPHICUM
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (REL. 14, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF THE SPORE COAT.
EMBL; M31737; G142763; -.
PIR; A43647; A43647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                 HUMAN ADENOVIRUS TYPE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 tippnylayd 422
                                                                                                                                                                                                                                                          377 fspdyltyee 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TEPPKYLHYD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOXIN; SPORULATION
                                                                                                                                                                                                                                                                                 3 FPPKYLHYDE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89008093
                                                    SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YP30_METTH
                                                                  STRAIN-DUGAN
                                                                                                                                                                                                                                                                                                                                CR72_BACTI
P21256;
                                                                                                                                                                                                                                                                                                                                                                                                        PROTOXIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLAMYDIA TRACHOMATIS.
LALSMID PLGV440, AND PLASMID PCHLI.
PRORARYOTA; GRACLLICUTES; SCOTOBACTERIA; RICKETTSIAS; CHLAMYDIALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGSNIA -> MALI (IN REF. 1 AND 4).
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MEDLINE; 90301796.
COMANDUCCI M., RICCI S., CEVENINI R., RATTI G.;
PLASHID 23:149-154(1990).
-!-PGR9-D IS REQUIRED FOR GROWTH WITHIN MANMALIAN CELLS.
EMBL, 201547; 640731; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 4; Length 332;
Pred. No. 6.01e+00;
5; Mismatches 2; Indels
                                                                                                                                                                                                              / Match 19.6%; Score 56; DB 11; Length 273; Local Similarity 58.3%; Pred. No. 6.01e+00; St. Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (APR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GP8D_CHLTR STANDARD; PRT; 332 AA.
P08788; P10554;
01.NOV-1988 (REL. 09, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
VIRULENCE PROTEIN PGP8-D (ORF8) (PROTEIN N-1/N-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1DEB5F46 CRC32;
STRAIN-MARBURG;
MEDLINE; 90221831.
MEDLINE; 90221831.
NUCLEIC ACIDS RES. 18:363-363(1990).
EMBL; X17205; 645718; --
PIR; 907880: 907880.
PIR; POTHETICAL PROTEIN; PLASMID.
SEQUENCE 273 AA; 30744 MW; FF211F2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
PLASMID-PLGV440; STRAIN-L1/440/LN;
MEDLINE; 88233998.
HATT C., WARD M.E., CLARKE I.N.;
NUCLEIC ACIDS RES. 16:4053-4067(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
PLASMID-PLGV440; STRAIN-L2;
MEDLINE; 89013892;
COMANDUCCI M., RICCI S., RAITI G.;
MOL. MICROBIOL. 2:531-538(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS TO C-TERMINUS.
PLASMID-PLGV440; STRAIN-L1/440/LN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 AA; 37918 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X06707; G473191; -.
EMBL; J03321; G455146; -.
PIR; S01180; S01180.
PIR; S01181; S01181.
PIR; S01920; S01920.
PIR; H37386; H37386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 typqkfmhflqe 236
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                                                                                                                                                                                                                                                                                                                          223 spkylfyasetg 234
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105 kylhfdesa 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                6 KYLHYDEET 14
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6
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P24881;
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YIHQ_ECOLI
P32138;
                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                 Matches
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                                                                                                                                                                                                      RESULT
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ID YIH
AC P32
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                                                                                                                                                                                                                             0
                                                                                                                                                               STRAIN-ATCC 11166;
LU T.Y.S., BULEY D.M.;
SUBMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1-FUNCTION: RUBISCO CATALYSES TWO REACTIONS: THE CARBOXYLATION OF D'RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYN'HETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRACMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANBOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: DEBULOSE 1,5-BISPHOSPHATE + 0(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-!- SPIBUNIT: IN CONTRAST TO FORM I GENES, THE FORM II RUBISCO ARE COMPOSED OF ONLY LARGE SUBUNITS (BY SIMILARITY).
-!- THIS PROTEIN IS ENCODED WITHIN THE FORM II RIBULOSE-BISPHOSPHATE CARBOXYLASE OPERON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                         CARDOLLES, G727418; -
PHOTOSYNTHESIS, CARBON DIOXIDE FIXATION; PHOTORESPIRATION;
LYASE; OXIDOREDUCTASE; MONOOXYGENASE; MULTIGENE FAMILY.
ACT_STE 191 191 BINDING OF CO(2) ACTIVATES THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168 / JH642;
KOBAYAȘHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S., SATO T.,
                                    01-OdT-1996 (REL. 34, CREATED)
01-OGT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OGT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CHIBULIOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN 2 (EC 4.1.1.39).
                                                                                                  RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).
PROKARYOTA: GRACILICUTES: ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 58.5 KD PROTEIN IN SPOIIIC-CWLA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
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MEDLINE: 95219086.
TAKEMARU K.-I., MIZUNO M., SATO T., TAKEUCHI M., KOBAYASHI Y.;
                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 | 3-PHOSPHO-D-GLYCERATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
Local Similarity 55.6%; Score 56; DB 8; L
Local Similarity 55.6%; Pred. No. 6.01e+00;
les 5; Conservative 2; Mismatches 2
                 458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINĘ: 96084975.
MEDIGUĘ C., MOSZER I., VIARI A., DANCHIN A.;
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MICROBIOLOGY 141:323-327(1995).
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                              RHODOSPIRILLACEAE.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 sfprqflhy 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACILLUS SUBTILIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TFPPKYLHY 10
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T 9
RBL2 RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQBA_BACSU
P45917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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GENETICS 130:471-498(1992).

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENXYME COMPLEX. CO I IS THE
CATALYTIC SUBUNIT OF THE ENXYME ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ** ERALLILALICARINGES.
-1-SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOMAINS.
-1-SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
EMBL, X54253; G559496; -...
PROSITE; PS00077; COXI.
OXIDOREDUCTASE; HEME: COPPER; MITOCHONDRION; TRANSMEMBRANE;
RESPIRATORY CHAIN; INNER MEMBRANE.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; ASCARIDIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN. CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)0 + 4 FERRICYTOCHROME C.
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0
                                                                                                                                                                                                             Length 510;
                                                                                                                                                                              Score 56; DB 11; Length olv. Pred. No. 6.01e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56; Ub 2,
No. 6.01e+00;
Thes 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON (HEME A3) (PROBABLE).
IRON (HEME A) (PROBABLE).
A6124BE2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRON (HEME A) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPPER B (PROBABLE),
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
                                                                                                                                                    510 AA; 58458 MW; 433165AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992 (REL. 21, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
GENE 165:GC37-GC51(1995).
-1- SIMILARITY: STRONG, TO B.SUBILLIS XKDE.
BMBL: D32216; G1217849; -.
SUBFILLST; BG11272; YQBA.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-BODY WALL MUSCLE, AND EGG;
MEDLINE; 92201635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58529 MW;
                                                                                                                                                                                                Query Match
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.6%;
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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PIR; A35726; A35726
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                                                                 STRAIN=S288C
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9
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                                                                                                                                                         NP_BIND
SEQUENCE
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GOMPELS U.A., NICHOLAS J., LAWRENCE G., JONES M., THOMSON B.J.,
MARTIN M.E., ESPATHIOU S., CRAXTON M., MACAULAY H.A.;
VIROLOGY 209:29-51(1995).
-: FUNCTION: PROVIDES THE PRECURSORS NECESSARY FOR DNA SYNTHESIS.
-: CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE DIPHOSPHATE + OXIDIZED
THIOREDOXIN + H(2)0 = RIBONUCLEOSIDE DIPHOSPHATE + REDUCED
                                                       ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE
01-OCT-1993 (REL. 27, CREATED)
1-CCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
HYPOTHETICAL 77.2 KD PROTEIN IN GLNA-FDHE INTERGENIC REGION (F678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY.
-:- SUBUNIT: HEPERODIMER OF LIARGE AND A SMALL CHAIN.
-!- SIMILARITY: HIGH TO OTHER BUKARYOTIC, PROKARYOTIC, AND VIRAL RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE LARGE CHAINS.
EMBL; X83413, G854007; ...
OXIDOREDUCTASE: DNA REPLICATION.
SEQUENCE 804 AA; 93352 MW; B599A3FD CRC32;
                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SECUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (EC 1.17.4.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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                                                                                                 STRAIN-K12 / MG1655;
MG1655;
MG1655;
MG1655;
MG1656;
MG1657;
MG187 G. II., BURLAND V.D., DANIELS D.L., BLAITNER F.R.;
NUCLEIC ACIDS RES. 21:3391-3398(1993).
EMBL; L19201; G304982;
PEMBL; L19201; G3049822.
ECOGENE; EG11843; Y.HQ.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                          Score 56; DB 11; Length 678; Pred. No. 6.01e+00; 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.6%; Score 56; DB 8; Length 804; 50.0%; Pred. No. 6.01e+00; artive 3; Mismatches 2; Indels
                                                                                                                                                                                                      678 AA; 77249 MW; 8D74E4AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                           804 AA
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                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        larity 50.0%;
Conservative
                                                                                                                                                                                                                           wery Match 49.6%; est Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                            RIBONUCLEOTIDE REDUCTASE)
                                                                                                                                                                                                                                                   4; Conservative
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(REL. 34, I
(REL. 34, I
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                                                                                                                                                                                                                                                                         589 plflhyedda 598
                                                                              ENTEROBACTERIACEAE
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5 PKYLHYDEET 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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P53914;
01-OCT-1996 (
01-OCT-1996 (
01-OCT-1996 (
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P52343;
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AC P5
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DT 01
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MEDLINE; 96109932.
MALLET L, BUSSEREAU F., JACQUET M.;
YEAST 11:1195-1209(1995).
-! SIMILARITY: TO AN A.AMBISEXUALIS HYPOTHETICAL PROTEIN (AC P54008).
EMBL; 246843, 6854505, -..
EMBL; 271408; E239944; -..
HYPOTHETICAL PROTEIN, ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (REL. 13, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) /
GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAAO032).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
HYPOTHETICAL 119.3 KD PROTEIN IN FPR1-TOM22 INTERGENIC REGION. YNL132W OR N1216 OR N1858.
SACCHAROWICES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA, FUNDI; ASCOMYCOTINA; HEMIASCOMYCETES.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -: SUBUNIT: HOWODIMER.
-: PATHWAY: ISOPRENE BIOSYNTHESIS.
-: SUBCELLIAR LOCATION: CYTOPLASMIC.
-: SIMILARITY: BELOMGS TO A FAMILY THAT GROUPS TOGETHER FPP SYNTHETASE, GGPP SYNTHETASE AND HEXAPRENYL PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                  Length 1056;
                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
NOMURA N., MIYAJIWA N., KAWARABAYASHI Y., TABATA S.;
SUBMITTED (MAR-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                 283 290 ATP (POTENTIAL).
1056 AA; 119347 MW; CF839C98 CRC32;
                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 11; I
Pred. No. 6.01e+00;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90170972.
WILKIN D.J., KUTSUNAI S.Y., EDWARDS P.A.;
J. BIOL. CHEM. 265:4607-4614(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                       EIN; ATP-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J05262; G182399; -. EMBL; D14697; G285965; ALT_INIT. EMBL; M29863; G182405; -.
                                                                                                                                                                                                                                                                                                                                                                                49.6%;
ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 8-353 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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Query Match
Best Local Similarity 33.3%; Pred. No. 8.97e+00;
Matches 4; Conservative 7; Mismatches 1; Indels 0;
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Release 2. Copyright Di	.1D John F. Collins, Biocomputing Research Unit. (c) 1993, 1994, 1995 University of Edinburgh, U.K. istribution rights by IntelliGenetics, Inc.
MPsrch_nn n.a	n.a. database search, using Smith-Waterman algorithm
Run on: Tue	Dec 2 14:43:20 1997; Maspar time 990.46 Seconds 1313.995 Million cell updates/sec
ular output not g	generated.
Title: >US Description: (1- Perfect Score: 118 N.A. Sequence: Comp:	>US-08-915-004-8 (1-1185) from US08915004.seq 1185 1 ATGAACAACTTGCTGTGCTGTAAAAATAAGCTGCTTATAA 1185 TACTTGTTGAACGACACGACATTTTTATTCGACGAATAT
Scoring table: TABLE Gap 6	SLE default .
Nmatch STD : Dbase	ise 0; Query 0
Searched: 362	62067 seqs, 549138275 bases x 2
Post-processing: Min	Minimum Match 0% Listing first 45 summaries
Database: embl 1:: 9:	bl-new3 1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV 9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
Database: gen	0.BCT3 21:BCT4 22:BCT5 23:BCT6 24 7:BCT10 28:BCT11 29:GEN1 30:GEN2
M 4 D II O K K W	38.1GEN3 32.HTG1 33.HTG2 34.HTG3 35.1NV1 35.1NV2 37.1NV3 38.1NV4 39.1NV5 40:1NV5 41.1NV7 42.1NV8 43.1NV9 44.1NV10 45.1NV11 46.1NAM1 47.1NV6 43.1NV9 43.1NV9 44.1NV10 45.1NV11 46.1NAM1 47.1NV1 48.1NAM3 49.1VRT1 50.1VRT2 51.VRT3 52.VRT4 53.1NT1 54.1NT2 55.1NT4 55.1NT1 54.1NT1 55.1NT4 57.1NT6 57.1NT8 57.1
	:SYN 95:UNA 96:VRL1 97:VRL2 98: 101:VRL6 102:VRL7 103:VRL8 104:
Database: gem 1. 1. 1. 1. Database: n-e	12: MAM 12: MAM 18: ROD
3	rtl
Statistics: Mean	11.245; Variance 4.362; sca
Pred. No. is the score greater that and is derived	the number of results predicted by chance to have a than or equal to the score of the result being printed, d by analysis of the total score distribution.

SUMMARIES

Pred. No.	n 2.40e-0 in 7.05e-0 kD 1.84e-	D 1.84e kD 1.90	d 1.90e	F 1.90e	D 1.34e	ie 1.34e	n 1.346 r 1.34e	cr 1.34	1.34e	346	en 1.346	ien 3.40e	ie. 1.346 or 3.40e	346 1.346 is 1.346	ran 1.346	1.346	Jan 1.346	Jan 3.406	r 1.346 fr 1.346	3.46	e ** 1.346	1.346	pate 5.01			30-0CT-1996		H. d their use to		
escrip	equence 5 from pate equence 5 from pate Oxytricha fallax 57	xytricha fallax Oxytricha fallax	xytricha fallax	arassius auratus	xytricha fallax	oxycitcha faitax .cuniculus SP17	.norvegicus inte I.musculus tumor	M.musculus tumor Mouse tumor necro	.cerevisiae chro H.sapiens LIPA o	H.sapiens LIPA ge S.cerevisiae fus2	Sequence 5 from P	cerevisiae nitr	luman LD78 beta g stagnalis mRNA	-	·# 6	っこ	-i ö		_ _	_ v	duen	fra	guence 13 from	norhabditis an DNA seque		PAT O.		ell,A. and Stotz,I galacturonases an 996;		
a ai	128278 S 128278 S OFU89259	•			_	N	ď.	MMTNFR2A MUSMTNFR2	r)	2	ı ır	,		3≤			0	01					FBU42380 I14734		ALIGNME	p DNA ent US 556983		tch,J.M., Powel f fungal polyge ease -A 5 29-OCT-199	Qualifiers	="unknown"
/ Length DB	7 215 57 5 215 57 4 354 111	4 354 1 354 1	1 354	1 1933 4	370	3/0 T	9 1380 9 9 1388 8	9 1388 1 9 1505 8	9 1761 6	9 1851 7 9 2492 6	2552 5	3021 6	9 3112 8 9 3177 4	3699 6	4561 3	17013 2	26923 28687	38586	40267	40397 6	90468	185775	105 56	37844 11 112762 11	0 1 1 1 1 1	215 e 5 from pa 4		es 1 to 215 A., Labavi nhibitors o fungal dis US 5569830	cation/	organism
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AUTHORS
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                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996,
                                                            tdttyrvnndsghnkyssanynyggnnvgaakthyythtnvsgadsktvtdsynasgtss 105
                                                                         snggtdgnrsgadsygssktamtsrnrt-gktannavdsrnmgdasvgsdkntkkhakns 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 ACACAGACAGCIGGCACACCAGIGACGAGIGICI - AIACIGCAGCCCGGIGI - GCAAGGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hvgaakthyythtnvsgadsktvtdsynasgtsssnggtdgnrsgadsygssktamtsrn 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgktannavdsrnmgdasvgsdkntkkhaknsadgkvgsknngdrnnrygtgtksnvsn 191
                                                                                                                                                                                                                                      30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ysrtascndkakkdgnttsswttdccnrtwgvcdtdttyrvnndsghnkyssanynyggn 71
                                        2; Gaps
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Oxytricha fallax

Oxytricha fallax

Bukaryotes; Alveolata; Ciliophora;

Bukaryotes; Stichotrichida; Oxytricha.

I (bases 1 to 334)

Doak,T.G., Doerder,F.P., Jahn,C.L. and Herrick,G.

A proposed superfamily of transposase genes: transposon-like
Best Local Similarity 18.8%; Score 32; DB 57; Length 215;
Matches 26; Conservative A. W. 2.40e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 57; Length 215;
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                                                                                                                                                                                                                           128278 215 bp DNA
Sequence 5 from patent US 5569830.
128278
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8 c 25 q
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                                                                                                                                                                                  ATCTTGGTCTTTGTTTTG 757
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Best Local Similarity 15.2%;
Matches 30; Conservative
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TITLE
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(pases 1 to 354)
Witherspoon, D.J., Doak, T.G., Williams, K., Seger, J. and Herrick, G. Selection on the protein-coding genes of the TBEI family of transposable elements in the ciliates Oxytricha fallax and O.
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11 FEB-1997) Oncological Science, University of Utah, School of Med. RmSC334, USA, UT 84132, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="this is a bulk sequence that was generated from PCR product that represents many transposon templates"
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13-WAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57KD zinc finger/protein chimera gene, partial
elements in ciliated protozoa and a common 'D35E' motif
Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
94134747
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3 (Dases 1 to 354)
Doak T.G., Williams, K., Witherspoon, D.J. and Herrick, G. Direct Submission
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Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

"A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common '035E' motif";

Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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/db_xref="piD:g1881676"
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/translation="HTRDLXKHLLKAHKKXXEXXXXXLKXLXKRKRREEXXXXXXXX
QAXEXXXVXXXRNXLXSEXTRIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVI
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13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
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Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;

Tyroposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";

Proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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"Selection on the protein-coding genes of the TBE1 family of
transposable elements in the ciliates Oxytricha fallax and O.
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Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora;
hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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                                                                                                                                                                                                                                                                                                           Length 354;
<1..>354
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/db_xref="PID:g1881676"
                                                                                                                                                                                                                                                                                                           Score 25; DB 111; Length 35:
Pred. No. 1.90e-01;
38; Mismatches 36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 CITIGGIGCCAGGCAAAITGICTACCAAGACACIAAG 637
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/strain="9D1"
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OFU89259 standard; DNA; INV; 354
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                                                                                                                                                                                                  XDHQYAYKVYPFNYL'
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2.1%;
Best Local Similarity 23.7%;
Matches 23; Conservative
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/note="this is a bulk sequence that was generated from
PCR product that represents many transposon templates"
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PCR product that represents many transposon templates"
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Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
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A proposed superfamily of transposase genes: transposan-like
elements in ciliated protozoa and a common 'D35E' motif
proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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hypotrichs; Stichotrichida; Oxytricha.
                                                     Submitted (11-FEB-1997) to the EMBL/GenBank/DDBJ databases.
Oncological Science, University of Utah, School of Med. Rm5C334,
USA, UT 84132, USA
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Doak, T.G., Williams, K., Witherspoon, D.J. and Herrick, G.
Direct Submission
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     Doak T.G., Williams K., Witherspoon D.J., Herrick G.;
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Sequence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
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2.4%; Score 28; DB 8; L4
Best Local Similarity 30.1%; Pred. No. 1.84e-03;
Matches 25; Conservative 33; Mismatches 24.
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/strain="9D1"
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Method: conceptual translation with partial peptide
sequencing. This sequence comes from Fig. 2"
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae;
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                                                                                                                                                                                                                                                  99 rgcdagrgaryhhyhdwargwbgydgwgcyykaayaagcwagmgarwyaswrtrygtaar 158
                                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 139069] from the original journal article. This sequence comes from Fig. 1. Location/Qualifiers
                                                                                                                                                                                                   Gaps
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Cohen,I., Shani,Y. and Schwartz,M.
Cohen,II., Shani,Y. and Schwartz,M.
Cloning and characteristics of fish glial fibrillary acidic protein: implications for optic nerve regeneration
J. Comp. Neurol. 334 (3), 431-443 (1993)
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                                                                                                        7 Match 2.1%; Score 25; DB 8; Length 354; Local Similarity 23.7%; Pred. No. 1.90e-01; Local 23; Conservative 38; Mismatches 36: Thable
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                                           Sequence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
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Pred. No. 1.90e-01;
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Best Local Similarity 77.8%;
Matches 35; Conservative
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                                                                                                                   Query Match
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LTCDLASLRGSNESLERQLREMEERFAIETAGYGYOTVARLEDEIQMKEEEMARHLQEY
QDLLNVKLALDIEIRTYRKLLGGEESRITVPVQNFTNLOFFRDEIQMKREEMARHLQEY
IVVRYVETROGEIIKESTTERKDLP"
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Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
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                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae;
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                                                                                                                                                                1 (bases 1 to 1933)
Glasgow, E. and Schechter, N.
Nucleotide sequence of a GFAP - like intermediate filament cDNA
from Goldfish retina
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Bukaryotae; intochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 115419)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="putative"
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Best Local Similarity 77.8%;
Matches 35; Conservative
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 /transl_table=6
/db_xref="PID:91881682"
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Length: 2554 bp Unfinished
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                                                                                                                                          * This sequence is unfinished. When sequencing is complete, the sequence data presented in this record will be replaced *by a single finished sequence with the same accession number. Location/Qualifiers
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Oncological Science, University of Utah, School of Med. Rm5C334,
USA, UT 84132, USA
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                                                                                                              *** WARNING: Phase 1 High Throughout Genome Sequence ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1997 (Rel. 51, Created)
13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein kinase gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doak T.G., Doerder F.P., Jahn C.L., Herrick G.;
"A proposed superfamily of transpoases genes: transposon-like
elements in ciliated protocoa and a common 'D35E' motif";
Proc. Natl: Acad. Sci. U.S.A. 91:942-946(1994).
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                                                                                                                                                                                                                                                                                                Length 115419;
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha.
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                                                                                                                                                                                                                                                                                                                                                        767 TCTTTGTTTTGATGTTTCCATAACTTCAGCAGCTGGAAAG 728
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Pred. No. 8.23e-01;
0; Mismatches 8;
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/strain="9D1"
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 Contig_ID:
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                                                                                                                                                                                                                                           'chromosome="22"
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sest Local Similarity 80.0%;
Aatches 32; Conservative
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/translation="HTRDLXKHLLKAXKKXXEXEXXXXXLKXLNKRKAREXXXXXXXX QAXEXEYVXXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVI
AXEXEYVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 bp DNA INV 14-MAR-1997 fallax 57kD zinc finger/protein kinase gene, partial cds.
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Oxytricha fallax.

Oxytricha fallax.

Eukaryotae; mitochondrial eukaryotes; Alveolata; Ciliophora; hypotrichs; Stichotrichida; Oxytricha.

I bases 1.0 370.)

Doak,T.G., Derder,F.P., Jahn,C.L. and Herrick,G. A proposed superfamily of transposase genes; transposon-like elements in ciliated protozoa and a common 'D35E' motif Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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Doak,T.G., Williams,K., Witherspoon,D.J. and Herrick,G.
Direct Submission
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Best Local Similarity 32.5%; Pred. No. 1.34e+01;
Matches 27; Conservative 28; Mismatches 27; Indels
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/db_xxef="PID:g1881682"
/transl_table=6
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                                                                                                                                                                                                                               Query Match 1.9%; Score 22; DB 8; Length 370; Best Local Similarity 32.5%; Pred. No. 1.34e+01; Matches 27; Conservative 28; Mismatches 27; Indels
                                                                                                                                                                     Sequence 370 BP; 116 A; 43 C; 48 G; 69 T; 94 other
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/codon_start=1
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Bristulf,J.
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Powell, E.E.
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Best Local Similarity 92.3%;
Matches 24; Conservative
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/note="3' untranslated region is identical for both 0.9 KB
AND 1.1 KB mRNAS"
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NLLEKREKTNFDPAEWGAKVDDRFYNNHAFQEHESEKCEAEEKSGSVTEEETPVLTID
SEDDKDKEEMAALKIQAAFRGHLAREDVKKIRTNKAEEETEENN"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-7AM-1993) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090

Hill, North Carolina, USA, 27599-7090

(bases I to 1256)
O'Rand,M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-APR-1994) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="alternate 5' untranslated region for 0.9 KB mRNA"
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736 CIGCIGAAGITAIGGAAACAICAAAACAAAGACCAAGAIA-IAGICAAGAAGAICAICCA 794
                                                                                                                                                                                                                               Orycfollagus cuniculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (Dases 1 to 1256)
Richardson, R.T., Yamasaki, N. and O'Rand, M.G.
Sequence of a rabbit sperm zona pellucida binding protein and localization during the acrosome reaction
95046885
                                                                                                                                      02-MAR-1995
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                                                                                                                                      MAM
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Pred. No. 1.34e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="New Zealand white"
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/clone_lib="Rabset"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="PID:9479084"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="testis"
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                               172 accwmytrrcmtchgarrtmacw 194
                                                  795 AGATATTGACCTCTGTGAAAACA 817
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                                                                                                                                 Occupiedlus SP17 gene.
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Best Local Similarity 69.6%;
Matches 39; Conservative
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European rabbit.
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Submitted (24-MAY-1993) Jesper Bristulf, Department of Neurochemistry and Neurochemistry and Neurochemistry and Neurochemistry and Neurosity, Stockholm University, Stockholm, S-106 91, Sweden Location/Qualifiers
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RORDFKSELELBGGEPVVLTCPLPVHPSDTSSSSSLESSSGVLFDGEPRWAVD
DTLWTLPAVQQDSGTYTCTFRNASHCEQMSLELKVFRVTEASFPLVSYLOISALSSTC
LLVCPDLKEFISSRTDGKIQWYKGSILLDKGNKKFLSAGDPTRLLISNTSMGDAGYYR
GVMTFTYERERISTSVAFTENVKFTTFEDRVTISPLETISPLTISNTSMGDAGYYR
GVMTFTYERFISVAFTSVAFTENVKFTSPEDRVTISPLETIVETYPCKFLGT
GTSSMTIVWMAANSTLYPTSVAFFECHHQYSRNDENVYEVSLIFPDPVTKEDLNT
DFKCVATNPFREFOSLAFTVKEVSSTFSWGIALAPLSLIILVVGAIWIRRRCKRQAGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae; Rattus.
1 (bases 1 to 1380)
Bristulf,J., Gatti,S., Malinowsky,D., Bjork,L., Sundgren,A.K. and
                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Vertebrata, Eutheria, Rodentia, Sciurognathi; Myomorpha, Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-1 stimulates the expression of type I and type II interleukin-1 receptors in the rat insulinoma cell line Rinm5F; sequencing a rat type II interleukin-1 receptor cDNA Eur. Cytokine Netw. 5 (3), 319-330 (1994)
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/db_xref="PID:g311408"
/db_xref="SWISS-PROT:p43303"
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                                                                                                                                                      RNINL1R2A 1380 bp RNA ROD R.norvegicus interleukin-1 receptor type 2.
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Pred. No. 1.34e+01;
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/cell_line="RINM5F"
124..1374
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US-08-915-004-8.rge

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/gene="murine tumour necrosis factor receptor 2"
/note="silent"
/replace="c"
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/strain="NOD"
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/db_xref="PID:9433831"
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                                                                               168 ctcggacaccgtgtgtgc 185
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Direct Submission
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PGQYYKHFCKKTSDPYCADCRASMTGVWNOPRTCLSCSSGSTDQVFTRACTKQUR
VCACEAGRYCALKTHSGSCRCCMRLSKCGPFGFQASSRAPNGNVLCKACAPGTFSDTT
SSTDVCRPHRTCSLIALPGNASTDAVCAPESPTLSALPRTLVYSQPEPTRSQPLDQEP
GPSQTPSILTSLGSTPILEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKK
PSCLQROAVYRHVPDEKSQDAVGLEQQHLLTTARSSSSSSSLESSARSADSRAPPGGHP
GDPDAKPSASSPKDEQVPFSQEECPSQSPYETTETLQSHEKPLPLGVPDMGMKPSQAGW
                                                                                                                                                    Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A. Allelic variation of the type 2 tumor necrosis factor receptor gene Manum. Genome 5 (11), 726-727 (1994)
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Submitted (26-NOV-1993) E.E. Powell, c/o John Todd, Level 6
Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford,
2 (bases 1 to 1388).
Powell,E.E., Wicker,L.S., Peterson,L.B. and Todd,J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is
linked to autoimmune diabetes in NOD mice
Unpublished
3 (bases 1 to 1388)
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/note="Phe to ile"
replace(921,"c")
/gene="murine tumour necrosis factor receptor 2"
/note="silent"
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replace(1317,"g")
/gene="murine tumour necrosis factor receptor 2"
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/note="Thr to Ile"
replace(489,"t")
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/gene="murine tumour necrosis factor receptor
/note="Ser to Thr"
replace(278, "t")
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/gene="murine tumour necrosis factor receptor /note="silent"
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/gene="murine tumour necrosis factor receptor
/note="ser to phe"
/pelace(1047, "t")
/gene="murine tumour necrosis factor receptor
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Pred. No. 1.34e+01;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                       /strain="NOD"
/chromosome="4 (distal region)"
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                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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Best Local Similarity 64.1%;
Matches 50; Conservative
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SSTDVCRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQPLDQEP
GPSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGVTSLGLLMLGLVNCFILVQRKKK
PSCLQRDAKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSSLESSASAGDRRAPPGGHP
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GDPDAKPSASPKDEQVPFSQEECPSQSPYETTETLQSHEKPLPLGVPDMGMKPSQAGW
FDQIAVKVA"
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Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.

Allelic variation of the type 2 tumor necrosis factor receptor gene

Mann., Genome 5 (11), 726-727 (1994)
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pggyvkhfcnkTsDTvCaDcEaSmyTQvwnQFRTCLSCSSSCSTDQveTRaCTKQQNR
vcaCeagryCalkThSGSCRQCmRLSKCGPGFGVASSRaPnGnvLCKACaPGTFSDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-NOV-1993) E.E. Powell, c/o John Todd, Level 6
Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK
2 (bases 1 to 1388)
Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is
Unpublished
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Vertebrata; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae;
108 tcagatgigcigitgctaagigtccicciggccaataigigaaacaittcigcaacaagac 167
                                                                  111 TCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTAACAAAACAACACTGTACAGCAAA 170
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/note="Ser to Thr"
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/note="silent"
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M.musculus tumor necrosis factor receptor 2 mRNA.
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variation

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Ouery Match
1.9%; Score 22; DB 118; Length 1388;
Best Local Similarity 64.1%; Pred. No. 1.34e+01;
Matches 50; Conservative 0; Mismatches 28; Indels 0; Gaps
                                       /gene="murine tumour necrosis factor receptor 2" /note="Ser to Phe" /replace="t" | 1047
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/note="silent"
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/gene="murine tumour necrosis factor receptor 2"
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• • Mutated OCIF, OCIF-CD
Mutated OCIF, OCIF-DD
Mutated OCIF, OCIF-CD
Mutated OCIF, OCIF-CB
Fragment of human OCI
Mutated OCIF, OCIF-CC
Mutated OCIF, OCIF-CC
OSteoclastogenesis in

0.00e+00 0.00e+00 0.00e+00 0.00e+00 1.46e-271 1.46e-271 1.58e-173 1.58e-173 1.58e-173 1.05e-29 1.05e-29 1.05e-29 1.05e-07 1.05e-07 1.05e-07 1.09e-05 1.09e-05 1.09e-05 1.09e-05

Human Natriuretic Pep Human Natriuretic Pep Oligonucleotide probe Base substituted E.co Oligonucleotide probe Base substituted E.co

133174 17331769 173318169 173318180 1736687 1736687 1736687 1736687 1736687 1736687 1736687 1736687 173687

Osteoclastogenesis in Mutated OCIF, OCIF-CP

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    n.a. database search, using Smith-Waterman algorithm

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factor coding sequence.
factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                               DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 8; Page 66-67; 183pp; Japanese.
This sequence encodes the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 10 mins at 56 deg.C., and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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Yasuda H;
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20-AUG-1996.
20-FEB-1995; JP-054977.
20-FEB-1995; JP-07508.
21-JUL-1995; JF-207508.
3NOW BRAND MILK PROD CO LTD.
GOTO M. Higashio K. Kobayashi F. Mochizuki S, McMaqawa N. Shima N, Tsuda E, Ueda M, Yano K, Yap-PSDB; R99924-25.
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Query Match

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                                                                                                                                                                                                            CAGGAAACGITICCICCAAAGIACCITCAITAIGACGAAGAAACCICICAICAGCIGIIG 120
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                          Indels 21; Gaps
  Pred. No. 0.00e+00;
0; Mismatches 0;
    Similarity 98.3%;
                        1185; Conservative
Best Local
Matches | 11
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 7. Page 122, 183pp, Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C19S in which the 19th Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation exchanges or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful in the control of bone resorption and therefore in the control of bone resorption of circum.
                                                               1081 gtcactcagagtctaaagaagaccatcaggttccttcacaggttcacaaatgtacaaattg 1140
                                                                                                      1060 GTCACTCAGAGTCTAAAGAACATCAGGTTCCTTCACAGCTTCACAATGTACAAATTG 1119
1000 ACCTIGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACT 1059
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                                                                                                                                                                                                                                           133161;
22-APR-1997 (first entry)
Mutated OCIF, OCIF-C19S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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T33161 standard; DNA; 1206 BP.
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                         ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacg 300
                                        gtttgcaaaagatgtccagatgggttcttctcaaatgagacgtcatctaaagcaccctgt 480
181 GTGTGCGCCCTTGCCCTGACCACTACTACAGAGACAGCTGGCACACCAGTGACGAGTGT 240
                                                                                                      280 CACAACCGCGTGTGCGAATGCAAGGAAGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA 339
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LT 3 T33165 standard; DNA; 1206 BP.

RESULT

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for bone resorption control, esp. Intentment of osteoporosis claim 39; Page 136-137; 183pp; Japanese. This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C23s in which the 23rd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-RAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. ocif is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
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                                               Mutated OCIF, OCIF-C23S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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29-AUG-1996.
29-AUG-1996.
R 20-FEB-1995; JP-054977.
PR 21-JUL-1995; JP-027508.
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S, Mory Goto M, Shima N, Tsuda E, Ueda M, Yano K, Yano M, Shima N, Tsuda E, Ueda M, Pano K, Yano M, Shima N, Tsuda E, Ueda M, Pano K, Yano M, Shima N, Tsuda E, Ueda M, Pano K, Yano M, Shima N, Tsuda E, Ueda M, Pano K, Yano M, Shima N, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Shima N, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Shima M, Tsuda E, Ueda M, Pano K, Yano M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M, Shima M
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89.0%; Score 1055; DB 27;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 1183; Conservative 0; Mismatches 2
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                         22-APR-1997
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                                                                                                                                         760 AACAAAAACCAAGATATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGC 819
                                                                                                                                                                         aaacggcaacacagctcacaagaacagactttccagctgctgaagttatggaaacatcaa 780
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Mutated OCIF, OCIF-C22S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
           CTGTGTGAGGAGGCATTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAAACTGGCTT
 |agaaaacacacaaattgcagtgtctttggtctcctgctaactcagaaaggaaatgcaaca
                                            cacgacaacatatgttccggaaacagtgaatcaactcaaaaatgtggaatagttacc
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20-FEB-1996, J00374.
20-FEB-1995; JP-054977.
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W09626217-A1.
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                                                                                         DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 36. Page 135-136; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C22S in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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89.0%; Score 1055; DB 27; Length 1206;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 1183; Conservative 0; Mismatches 2; Indels 21;
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                                             Yasuda H;
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                     Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
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(SNOW ) SNOW BRAND MILK PROD CO LID.
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C20S in which the 20th Cys residue in the mature ocif protein is substituted by Ser. The OCIF of the invention and molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto eation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                aacaaagaccaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
                       700 AAACGGCAACACCACCACAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAA 759
                                                              880 AGCITACCGGGAAAGAAAGTGGGGAGCAGAAGACATTGAAAAAACAATAAAGGCATGCAAA
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F, Mochizuki S,
Ueda M, Yano K,
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
21-JUL-1995; JP-207508.
CSNOW, HIGASHIO K, KODAYASHI F, GOLO M, HIGASHIO K, KODAYASHI F, NAKAGGWW N, SHIMM N, TSUGM E, UE
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T33162 standard; DNA; 1206 BP
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in the treatment and prevention of disorders of bone resorption,
                                                                                                                                                                                                                                                                                                                        2; Indels 21;
                                                                                                                                                                                                         89.0%; Score 1055; DB 28; Length 1206; 98.1%; Pred. No. 0.000+00; vative 0; Mismatches 2; Indels 21;
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P-PSDB, R99933.

DNA ehcoding osteoclastogenesis inhibitory factor protein - useful for bohe resorption control, esp. treatment of osteoporosis (lam | 33; Page 134-135; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteo-clastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutated version of CCIF of the invention. This sequence encodes OCIF-C21S in which the 21st Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. Cors of the control of bone resorption and therefore control of the resorption and therefore the control of bone resorption and therefore control of the resorption and therefore the control of the protein is a resorption.
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Mutated OCIF, OCIF-C21S, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                    CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGAC 999
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Morinaga T;
Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 88.9%; Score 1053; DB 27; Length 1206; Local Similarity 98.0%; Pred. No. 0.00e+00; hes 1182; Conservative 0; Mismatches 3; Indels 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goto M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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20-FEB-1995; JP-054977,
21-JUL-1995; JP-207508;
(SNOW|) SNOW BRAND MILK PROD CO LTD.
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                                                         181 gtgtgcgcccttgccttgaccactactacagacagctggcacaccactgacgagtgt
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 60; Page 143-144; 183pp. Japanese.

Claim 60; Page 143-144; 183pp. Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CL in which amino acids 379-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                             22-APR-1997 (first entry)
Mutated OCIF, OCIF-CL, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LFD.
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                                                                    T33172 standard; DNA; 1200 BP
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                                                                                                                                                                         osteoporosis; ss.
1180 TTATAA 1185
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Mutated OCIF, OCIF-CBst, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                          Location/Qualifiers
1..63
JT 8
T33178 standard; DNA; 1182 BP.
                            (first entry)
                                                                                                       64..1179
                                                                                                                                           29-AUG-1996.
20-FEB-1996, JO0374.
20-FEB-1995, JP-054977.
21-JUL-1995, JP-207508.
                                                                                                                         'product = OCIF-CBst
                                                        osteoporosis; ss.
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                                   Morinaga T;
Yasuda H;
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                             F, Mochizuki S,
Ueda M, Yano K,
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Pred. No. 0.00e+00;
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        LTD.
(SNOW) ) SNOW BRAND MILK PROD CO
GOLO M, Higashlo K, Kobayashi
Nakagawa N, Shima N, Tsuda E,
WPI; 96-402320/40.
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al Similarity 98.0%;
1156; Conservative
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New human tumour necrosis factor receptor - used to develop prods.

To treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation

Claim 1; Fig 1; 59pp: English.

The receptor binds to TNF, and in particular, TNF-beta.

The receptor and for ligands for antegonists and agonists of the receptor and for ligands for the receptor. Such agonists may be used to inhibit the growth of tumours, to stimulate cellular differentiation, to mediate the immune response and anti-viral response, to requiate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat uutoimmune diseases, inflammation, septic shock, to inhibit graft.

Contact of the receptor and to prevent apoptosis.

Sequence 1173 BP; 374 A; 277 C; 265 G; 257 T;
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721 aaacggcaacacagctcacaagaacagactttccagctgctgaagttatggaaacatcaa 780
                                    700 AAACGGCAACACACACACAAAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAA 759
                                                                            781 aacaaagaccaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
                                                                                                                                                          gtgcagcggcacattggacatgctaacctcaccttcgagcagcttcgtagcttgatggaa 900
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                                                                                                                                                                                                                                    940 CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGCGAATAAAAATGGCGACCAAGAC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor receptor.
Tumour necrosis facor; INF; receptor; INF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
                                                                                                  1021 accttgaagggcctaatgcacgcactaaagcactcaaagacgtaccactttcccaaaact
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T35475 standard; cDNA; 1173 BP.
T35475;
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15-MAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
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P-PSDB; R99357.
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Length 1173;

DB 28;

85.8%; Score 1017;

Query Match

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503 AGAAAGGAAATGCAACACACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAT
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Best Local Similarity 98.0%;
Matches 1150; Conservative
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for bone resorption control, esp. treatment of osteoporosis
Claim 42; Page 137-138; 183pp; Japanese.
This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-DCR1 in which amino acids 2-42 of the mature
protein have been deleted. The OCIF of the invention has a molecular
whight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
non-reducing conditions. The protein is adsorbed onto cation-exchangers
or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
in the control of bone resorption and therefore in the treatment and
prevention of disorders of bone resorption, e.g. osteoporosis.
Sequence 1083 BP; 352 A; 250 C; 246 G; 235 T;
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                                                                 tytcactcagagtctaaagaagaccatcaggttccttcacagcttcacaatgtacaaatt 1140
1000 ACCTTGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCA-AAAC 1058
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T33166 standard; DNA; 1083 BP.
T33166;
22-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR1, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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Ueda M,
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21-FEB-1995; JP-05497.
21-JUL-1995; JP-207508.
(SNOW ).SNOW BRAND MILK PROD CO LTD.
GOLO M, HIGABILO K, KODBYASAHI F, MOC
NAKAGAWA N, Shima N, Tsuda E, Ueda M,
WPI; 96-402320,40.
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accactttcccaaaactgtcactcagagtctaaagaagaccatcaggttccttcacagct 1000
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 gtggaatagatgttaccctgtgtgaggaggcattcttcaggtttgctgttcctacaaagt 520
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Mutated OCIF, OCIF-CC, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
             |agagtgtagagagataaaacggcaacacagctcacaagaacagacttccagctgctga
                                                                                                                                      AGAGTGTAGAGGATAAAACGGCAACACAGCTCACAAGAACAGACTTTCCAGCTGCTGA
                                                                                                                                                                                DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 63; Page 144-145; 183pp; Japanese.
                                                       ttacgcctaactggcttagtgtcttggtagacaatttgcctggcaccaaaqtaaacgcag
                                                                                623 TTACGCCTAACTGGCTTAGTGTCTTGGTAGACAATTTGCCTGGCACCAAAGTAAACGCAG
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Yasuda H;
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a M, Yano K,
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Ueda M,
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) | NOWW BRAND MILK PROD CO LT GOLO M. Higgshio K. Kobayashi F. Nakagawa N. Shima N. Tsuda E. De
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T33179 standard; DNA; 1056 BP.
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P-PSDB; R99943.
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This sequence encodes a mutated version of the full length softeoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CC in which amino acids 331-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. ocif is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Ueda M,
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M9962617-A1.
29-AuG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTI GOCO M, Higashio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Ue
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T33179 standard; DNA; 966 BP.
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Claim 45; Page 138-139; 183pp; Japanese.
This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-DCR2 in which amino acids 43-84 of the mature
protein have been deleted. The OCIF of the invention has a molecular
weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
non-reducing conditions. The protein is adsorbed onto cation-exchangers
or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
in the control of bone resorption and therefore in the treatment and
prevention of disorders of bone resorption, e.g. osteoporosis.
Sequence 1080 BP; 357 A; 243 C; 236 G; 244 T;
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901 agcttaccgggaaaggaaagtgggagcagaagacattgaaaaaacaataaaggcatgcaaa 960
                                                                                                                  940 CCCAGIGACCAGAICCIGAAGCIGCICAGIIIGIGGCGAAIAAAAAIGGCGACCAAGAC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutated OCIF, OCIF-DCR2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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i F, Mochizuki S,
Ueda M, Yano K,
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                                                                                                                                                                                                                                                          Location/Qualifiers 1..63
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20-FEB-1995; JP-05497.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LT GOLO M, Higsshio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Ue P-PSDB; R99937.
                                                                                                                                                                                                                                                                                                                                                                             .T 12
T33167 standard; DNA; 1080 BP.
T33167;
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W09626217-A1.
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429 ttccggaaacagtgaatcaactcaaaaatgtggaatagatgttaccctgtgtgaggaggc 488
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Yasuda H;
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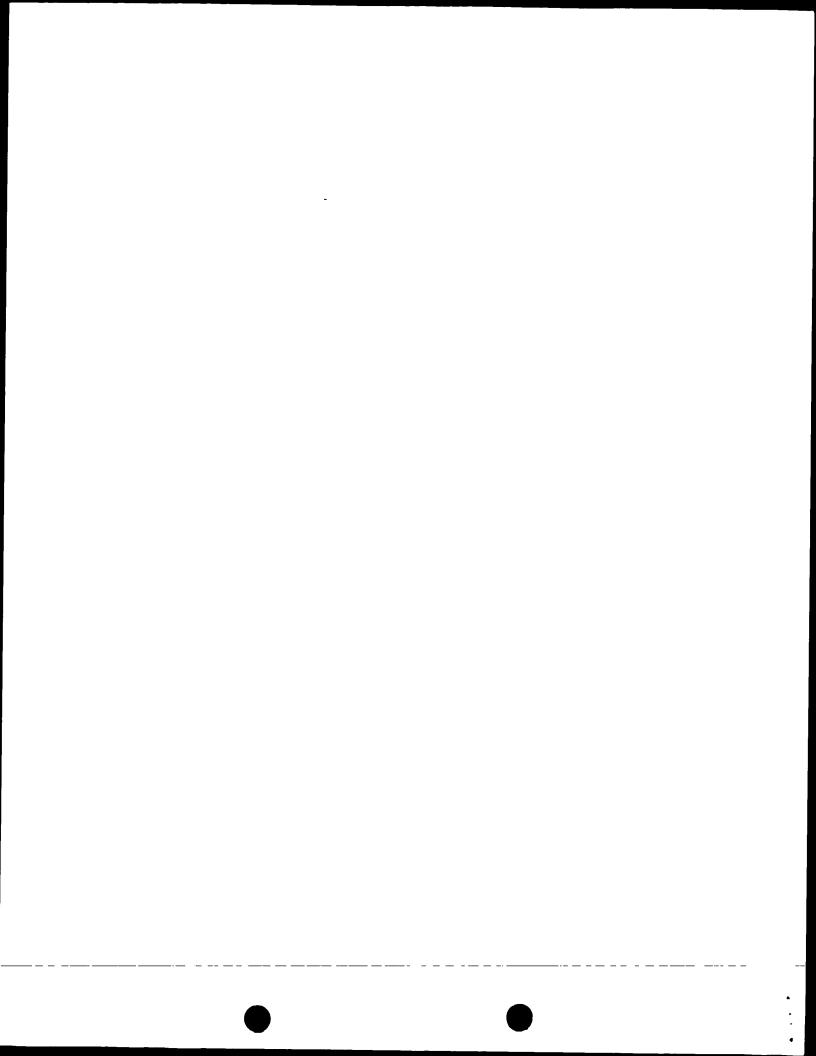
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                             This sequence encodes a mutted version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CSph in which amino acids 298-380 of the mature protein have been deleted and replaced by Ser-Leu-Asp. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or hearing and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the prevention of disorders of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 966;
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Pred. No. 0.00e+00;
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Best Local Similarity 97.8%;
Matches 932; Conservative
Claim
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for bone resorption control, esp. treatment of osteoporosis
Claim 48; Page 139-140; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DCR3 in which amino acids 85-122 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. or 31 in the control of bone resorption and therefore in the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                     841 gtgcagcggcacattggacatgctaacctcaccttcgagcagcttcgtagcttgatggaa 900
                                                                                                                                      820 GIGCAGCGCCACATTGGACATGCTAACCTCCACCTTCGAGCAGCTTCGTAGCTTGATGGAA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutated OCIF, OCIF-DCR3, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      588
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760 AACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGC 819
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0
                                                                                                                                                                                                           901 agcttaccgggaaaggaaagtgggagcagaagacattgaaaaaacaataaaggc 953
                                                                                                                                                                                                                                               prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 1080 BP; 351 A; 259 C; 233 G; 237 T;
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Yasuda H;
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20-FEB-1995; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
NAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K,
WPI: 96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 765; DB 27;
Pred. No. 0.00e+00;
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Best Local Similarity 100.0%;
Matches 765; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1997 (first entry)
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Mutated OCIF, OCIF-DDD2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                   852
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caagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagcgtgcagcgg
                                                                                                                                       cacattggacatgctaacctcaccttcgagcagcttcgtagcttgatggaaagcttaccg
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Yasuda H;
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20-FEB-1995; JD-054977.
20-FEB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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T33171 standard; DNA; 984 BP
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                                                                                                                                                                                                                                                                                            121 IGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACC 180
                                                                                              1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                    Indels 21; Gaps
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                                                                                                                                                                           61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg
                                                                                                                                                                                                                                                                                                                                                                         181 GTGTGCGCCCTTGCCCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                   241 ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
                                                                                                                                 1 ATGAACAACTIGCIGIGCIGCGCGCCCGTGTTTCIGGACAICTCCCATIAAGIGGACCACC
                  Length 984;
Score 671; DB 27; L
Pred. No. 0.00e+00;
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              Query Match
Best Local Similarity 97.4%;
Matches 797; Conservative
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Distribution rights by IntelliGenetics, Inc.
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(1-1185) from US08915004.seq
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zc52h03.rl Soares sen 0.00e+00
yw23g12.rl Homo sapie 5.01e-07
ma38f10.rl Soares mou 2.66e-04
Rice cDNA, partial se 2.66e-04
Rice cDNA, partial se 2.66e-04
yw62a02.rl Homo sapie 1.22e-05
Human fetal brain cDN 2.66e-04
TgESTry27b03.rl Txxxp 2.66e-04
TgESTry27b03.rl Txxp 2.66e-04
TGESTry27b01.rl Homo sapie 1.2e-05
yx47d01.rl Homo sapie 1.2e-05
yx47d01.rl Homo sapie 2.66e-04
ye07c04.rl Homo sapie 2.66e-04
yw772e10.rl Homo sapie 2.66e-04
yd72e10.rl Homo sapie 2.66e-04
yd72e10.rl Homo sapie 2.66e-04
yd72e10.rl Homo sapie 2.66e-04
yd72e10.rl Homo sapie 2.66e-03
H. sapiens partial cD 5.06e-03
yu6040.sl Homo sapie 5.06e-03
yu60410.sl Homo sapie 5.06e-03
Human fetal brain cDN 5.06e-03
rhuman fetal brain cDN 5.06e-03
rhuman fetal brain cDN 5.06e-03
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rk14f03.rl Soares mou 5.06e-03
xy44d05.sl Stratagene 5.06e-03
ze07d08.rl Soares mou 5.06e-03
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179:EST179
184:EST184
189:EST189
194:EST194
178:EST178 1
183:EST183 1
188:EST188 1
193:EST193 1
                                                                                                                                                  scale 5.941
177:EST177 1
182:EST182 1
187:EST187 1
192:EST192 1
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H8769

H172414

M10583

AA100384

H14106

C14856

C14856

C14856

N61165

N61165

N61157

T74804

T74804

T74804

T74804

T74804

T74804

T74803

W10113

W10113

W1013

175:EST175 176:EST176 1
180:EST180 181:EST181 1
185:EST185 186:EST186 1
190:EST190 191:EST191 1
195:EST195 196:EST196 1
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Match Length
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2 103:EST103 104:EST104 7 108:EST108 109:EST109 2 13:EST113 114:EST114 2 123:EST123 124:EST124 7 128:EST123 124:EST124 7 128:EST123 129:EST124 7 138:EST123 134:EST124 7 138:EST138 139:EST134 7 138:EST138 139:EST134 7 138:EST143 144:EST144 7 158:EST148 149:EST149 7 158:EST168 159:EST159 7 168:EST168 169:EST154 7 168:EST168 169:EST164 7 168:EST168 169:EST164 7 168:EST163 174:EST164

102:EST102 I 107:EST107 I 117:EST117 I 122:EST127 I 122:EST127 I 137:EST137 I 137:EST137 I 142:EST147 I 147:EST147 I 147:EST167 I 167:EST167 I 167:EST167 I

100:EST100 101:EST101 10 105:EST105 106:EST106 101 110:EST110 111:EST116 111 120:EST110 111:EST116 111 120:EST120 121:EST121 12 130:EST120 121:EST121 12 130:EST130 131:EST131 13 135:EST130 131:EST131 13 135:EST140 141:EST141 14 145:EST145 146:EST146 14 150:EST150 151:EST146 14 160:EST150 151:EST161 16 160:EST150 161:EST161 16 160:EST160 161:EST161 16

Database:

AA098806 N96353 AA100749 N38845

4474 4491 4496 500 514 551

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zc52h03.rl Soares senescent fibroblasts NbHSF Homo sapiens CDNA clone 325973 5'.
AA037313
91512420 DEFINITION ACCESSION NID KEYWORDS

862 421

921

22-NOV-1995

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Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ostelohthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archorta; Primates; Catarrini; Hominidae; Homo.

[ bases 1 to 346)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Washur-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human clone=253126 primer=M13RPl library=Morton Fetal Cochlea vector=pBluescript SK host=SOLR cells (kanamycin resistant) Ksitel=Ecool Rsite2=XhoI The cDNA was oligo (dT) primed with an XhoI restriction enzyme recognition site and an 18 base poly dT sequence. For the 5' end, the synthesized cDNA termini were treated with T4 DNA polymerase and EcoRI adaptors were ligated to the blunt ends. adaptor linker: GAATTCGGCACGAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: estewateou.www.row.
High quality sequence stops: 278
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1085 TCAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTTTAGAAATGA 1144
                                                                                             422 titcgiagcitgaiggaaagcitaccgggaaagaaagaaagigggagcagaagacatigaaaaa 481
                                                                                                                                                                                       482 acaataaaggcatgcaaacccagtgaccagatnotgaagctgctcagtttgtgggcgaata 541
                                                                                                                                                                                                               1 tcaggttccttcacagcttcacaatgtacaaattgtatcagaagttatttttagaaatga 60
                                                                                                                                                                                                                                                                                                            804 CCTCTGTGAAAAAGAGCGGCAGCGGCACATTGG-ACATGCTAACCTCACCTTCGAGCAGC
           cototgtgaaaacagcgtgcagcggcacattgggacatgctaacctcaccttcgagcagc
                                                                                                                                            863 IT-CGTAGCTTGATGGAAAGCTTACCGGGAAAGAAAGTGGGGAGCAGAAGAAAAA
                                                                                                                                                                                                                                                                               542 aaaaatggcgaccaaganaccttgaaagggnctaatgcacgcacttaagcactcaa 597
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 3.89e-165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="253126"
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les 101; Conservati
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wastson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INSECT Length: 1203 Std Error: 0.00
Seg primer: -28M13 rev2 from Anersham
High quality sequence stop: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTAAAGCACCCTGTAGAAAACACACAAATT-GCAGTGTCTTTGGTCTCCTGCTAACTCA 503
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                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 602)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
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98.78;
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est Local Similarity 98.7%;
atches 588; Conservative
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                                                                                                                                                                                                                                                Unpublished (1995)
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                                                                                     REFERENCE
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                                                                                                             AUTHORS
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DEFINITION

ACCESSION

NID KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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AA100384 300 bp mRNA EST 28-OCT-1996 zn46h08.rl Stratagene HeLa cell s3 937216 Homo sapiens CDNA clone 550527 5'. AA100384 g1646757
                                                               Washighton University School of MedicineP Washighton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infofilmage.llnl.gov) for further information. Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -20M13 rev2 from Amersham
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vortebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 300.

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,
Wasterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Unpublished (1995)
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/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22; DB 148;
Pred. No. 2.66e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.9%;
Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Conservative
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                            ..267
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                  Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 504)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullann,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Wasterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 267)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W10583 267 bp mRNA EST 05-SEP-1996
masH10.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 313003 5'
%inniar to gb:219554 VIMENTIN (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High qulity sequence stops: 299
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                             172414 EST 01-MAR-1995 yc72a07.rl Homo sapiens cDNA clone 86196 5' similar to gb:X54486_rnal PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                            human clone=86196 library=Stratagene liver (#937224)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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121 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.0%;
Best Local Similarity 73.9%;
Matches 34; Conservative
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g686935
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BASE COUNT ORIGIN

FEATURES

Mus.

REFERENCE AUTHORS

TITLE

ORGANISM

DEFINITION

RESULT

ACCESSION

KEYWORDS

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Gaps

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LOCUS C14856 360 bp mRNA EDEFINITION Human fetal brain cDNA 5'-end GEN-093D09.
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/clone="163472"
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High quality_sequence_stops: 313
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WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.9%;
Best Local Similarity 77.8%;
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                          /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
epitheliold carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni_ZAP XR
Vector. -5' adaptor sequence: 5' GAATICGGCACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3' -
/clone="550527"
/csx="female"
/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 330)
Sasski, T. and Minobe, Y.
Rice cDNA from callus
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                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (strain Nipponbare, ) callus cDNA to mRNA.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 gtaacttcattgcaaccacgaaacctgtaatacgctgtacagtaacaagtgt 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 GTACCTICATTATGACGAAGAACCTCTCATCAGCTGTTGTGTGAGAATGT 132
                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 183; Length 300; Pred. No. 2.66e-04;
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1.9%; Score 22; DB 13; Length 330;
Best Local Similarity 70.4%; Pred. No. 2.66e-04;
Matches 38; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                       2 others
                                                                                                                                                                                                                                                           /dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yuzo Minobe
National Institute of Agrobiological Resources
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                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
/strain="Nipponbare"
High quality sequence stop: 258.
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47 c 83 g
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     51 g
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Best Local Similarity 71.2%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                     43 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Japan 305
Phone:0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                  <1..>300
                                       1.300
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                                                                                                                                                                                                                                                                                                                     109 a
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AUTHORS
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Ouble-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library went constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which coccurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter. basal ganglia, thalamus, cerebellum, midbrain, pons and medulla.
                                                                                                                                               ym62a05.rl Homo sapiens cDNA clone 163472 5' similar to SP:S32367 832367 SAPA-SNAP PROTEIN - ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata: Vertebrata; Gnathostomata; Osteichthyes;
Barcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 344)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                       Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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1034 GAGTGCTTTAGTGCGTGCATTAGGCCCTTCAAGGTGTCTTGGTCGCCATTTTTT 981
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 1.22e-09
0; Mismatches
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                                                                                                                                                                                 Direct Submission
Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Ctsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd; 463-10 Ragasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
2 (sites)
Fujiwara_T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Syushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Matanabe,T., Meckawa,H., Nakamura,Y. and Takahashi,E.
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Source: David Sibley, Washington University
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Location/Quallifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-1996
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Ajioka,J.A., Aslett,M.A., Dietrich,N., Dubuque,T., Kucaba,T., Marra,M., Sibley,L.D., Wan,K.L. and Waterston,R.A.
Unpublished (1996)
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TGESTZY27b03.rl Toxoplasma gondii cDNA clone tgZy27b03.rl 5'
Similar to SW:EFIA_PLAFK 000080 ELONGATION FACTOR 1-ALPHA ;.
N61165
                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
Fujiwara,T.
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Eukaryotae; mitochondrial eukaryotes; eukaryote crown grou
Alveolata; Apicomplexa; Coccidia: Eimeriida; Sarcocystida;
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                           EST(expressed sequence tag); Human fetal brain.
Homo sapiens fetus brain cDNA to mRNA, clone:093D09.
Homo sapiens
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Pred. No. 2.66e-04;
5; Mismatches 17; Indels
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/clone="093D09"
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type-"brain"
83 c 75 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.7%;
Matches 34; Conservative
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1 (bases 1 to 385)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                         AAU87288 385 bp mRNA EST 23-OCT-1996 mol1d06.rl Life Tech mouse embryo 10 5dpc 10665016 Mus musculus CHUMAN); gb:M25949 Mouse carbonic anhydrase II (MOUSE);. AAO87288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/note="Vector: pCMV-SPORI2; Site_1: Sall; Site_2: NotI;
Cloned unidirectionally. Primer: Oligo dT. 10.5dpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                            266 gtttcgttggtgataaacatggtggagaagtccaccaacatgagctggtacaagggcaag 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Life Tech mouse embryo 10 5dpc 10665016" /dev_stage="10.5dpc embryos"
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WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 2.66e-04;
0; Mismatches 3; Indels (
                                                                                                                                                                                  Length 371;
                                                                                                                                                                            Score 22; DB 99; Length 371
Pred. No. 2.66e-04;
0; Mismatches 19; Indels
     gondii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
/organism="Toxoplasma
/clone="tgzy27b03.rl"
/strain="RH"
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Best Local Similarity 89.3%;
Matches 25; Conservative
                                                                                                                                                                            Ouery Match 1.9%;
Best Local Similarity 68.3%;
Matches 41; Conservative
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ACCESSION

KEYWORDS

JOURNAL

AUTHORS JOURNAL

TITLE COMMENT FEATURES

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/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I: - oligo(dT) primer [5] and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst and the analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analyst analys
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1 (bases 1 to 410)

1 Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Huthman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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High quality sequence stops: 212
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human clone=85063 library=Stratagene liver (#937224)
vector=pBluescript SK host=50LR cells (kanamycin resistant)
primer=M13RP1 Rsitel=ECORI Rsitel=ENOI Cloned unidirectionally.
Primer: 01490 dT. Hepatectomy from normal 49 year old male
caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; 5'
adaptor sequence: 5'-GAATGGGCACGAG-3'; 3' adaptor sequence:
5'-CTCGAGTFTTTTTTTTTTTTTTTT-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares mouse embryo NbME13.5 14.5"
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T74804
g691479
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Pred. No. 2.66e-04;
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                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                     High quality sequence stop: 349.
Location/Qualifiers
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/dev_stage="13.5-14.5
/lab_host="DH10B"
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                                                  Putative full length read
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WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="unknown"
                                                                                                Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.9%;
Best Local Similarity 72.0%;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (20-FEB-1993) Genzentrum Muenchen, Laboratorium fuer
molekulare Biologie, Am Klopferspitz 18a, 8033 Martinsried,
Germany. E-mail: obermaier@vms.biochem.mpg.de
2 (bases 1 to 387)
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                                                                                                                                                                                    03-FEB-1994
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
                                                                                                                                                                                                                    H. sapiens partial CDNA sequence; clone H23G03; single read 221693
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 |cagtgacccaaacctgaacctgctcagttt 283
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SP:TCPB_MOUSE P80314 T-COMPLEX PROTEIN 1, BETA SUBUNIT
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( bases 1 to 442)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                     T71938 442 bp mRNA EST 16-MAR-1995 ye07c04.rl Homo sapiens cDNA clone 117030 5' similar to gb:x54486_rna1 PLASMA PROTEASE CI INHIBITOR PRECURSOR (HUMAN);.
 IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS N21157 453 bp mRNA EST 19-DEC-1995
DEFINITION yx47d01.s1 Homo sapiens CDNA clone 264865 3' similar to
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 1.22e-05;
0; Mismatches 8; Indels
                                                                                                                                                  6; Length 410;
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                                                                                                                                              Query Match 1.9%; Score 22; DB 6; Lk Best Local Similarity 80.6%; Pred. No. 2.66e-04; Matches 29; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                         163 aagatgatgatccaagaaaatgaaatttgtgaaaac 198
                                                                                                                                                                                                                                                              781 AAGAAGATCATCCAAGATATTGACCTCTGTGAAAAC 816
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                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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117 c
                                                                     /clone="85063"
57 c
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Best Local Similarity 79.5%;
Matches 31; Conservative
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                                        1..410
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CEYWORDS
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Dubman clone=264865 primer=m13 -40 forward library=Soares melanocyte 2NbHM vector=pT7T3D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) Rsitel=not I Rsitel=Eco RI Male. Ist strand cDhA was primed with a Not I - oligo(dT) primer ist stranded cDhA was primed with a Not I - oligo(dT) primer ist stranded cDhA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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Deuterosticmia: Chordata; Vertebzata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tertapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 453)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Ruclan,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Best Local Similarity 77.5%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <1..>453
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zr35a03.rl Soares NhH zr35a03.rl Soares NhH ma38f10.rl Soares mou human STS SHGC-13782 Human STS UT1054.

MM5835 G10922 HUMUT1054

5740 Arabidopsis thal ma42d03.rl Soares mou mp53f02.rl Soares 2Nb

AT4774 MM1135

mp53f02.r1 Soares 2 mp53f02.r1 Soares 2 Human STS UT5145. human STS MR4116.

MMAA17046 AA117046

HUMUT5145

NhH NhH NhH

zr47g08.rl Soares zr47g08.rl Soares

AA233719 HS1151638 AA195113 AA195113

Match Length DB

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Listing first 45 summaries
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Perfect Score:
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MMAA12293

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AA213094 AA213094 AA020160

D. melanogaster STS d mb83g02.rl Soares mou IB862 Infant brain, B

DM122E4S MM05110 T03759

25363 25

mh49h05.rl Soares mou

15713 Arabidopsis tha 6. human STS SHGC-10698. 6. zr5541.s1 Soares NhH 6. zt30e09.s1 Soares mou fmt16h02.r1 Soares mou mt16h02.r1 Soares mou 21638 Arabidopsis tha 6

AA126852 AT58413 G1347657 AA235526 MAAA78725 AA118725 AA126432

390 8 2 394 77 4 400 40 0 4 17 82 1 421 66 2 469 103 469 11 2 510 75 2

mu06e03.rl Soares mou zp89h01.rl Stratagene

zn88ell.sl Stratagene

mu06e03.rl Soares mou

va88d03.rl Soares pre mj55b12.rl Soares mou my55b12.rl Soares mou mv56h03.rl Soares

mv56h03.rl Soares mou human STS WI-7816.

MMAA51619 AA217740 G06714

MMAA60123

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AA233719 463 bp mRNA EST 28-FEB-1997 zz47408.rl Soares NhHMPu Sl Homo sapiens cDNA clone 666590 5' 4A233719 g1856711
                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46); Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucabb,T., Leo,M., Lennon,G., Marra,M. Parsons,J., Rikfin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Wilson, R.
                                                                                                                                          human.
                     LOCUS
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                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                  ACCESSION
                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                        AUTHORS
                                                                                                             KEYWORDS
RESULT
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query

Result

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//note=Torgan: mixed (see below); Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site]: Not I; Site=2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.W.A.G.E. clones 260232-265223, 340488-345479, and 44848-4489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 448.
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06-MAR-1997 (Rel. 51, Last updated, Version 1)
2r47908.rl Soares NhHMPu S1 Homo sapiens cDNA clone 666590 5'.
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertębrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 1; Indels
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                                                                  est@watson.wustl.edu
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Best Local Similarity 99.6%;
Matches 256; Conservative
                      Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.
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/note="Organ: mixed (see below): Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZNBHW, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction
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Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                   Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 53108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -28ml3 rev2 ET from Amersham High
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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WashU-Merck EST Project";
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Local Similarity 99.6%;
nes 256; Conservative
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TITLE JOURNAL

COMMENT

FEATURES

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/ncre="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus" /lab_host="DH108"
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
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03-MAR-1997 (Rel. 51, Last updated, Version 2)
ma38f10.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 313003 5'
similar to 9b:219554 VIMENTIN (HUMAN);
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Dubbque T., Galsel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptce M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the TMACE Consortium (info@image.llnl.gov) for further information. High quality sequence stop: 257.
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2r35a03.rl Soares NhHMPu Sl Homo sapiens CDNA clone 665356 5'
AA195113
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 26 1810
Enail: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 530;
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Pred. No. 1.10e-102;
0; Mismatches 0;
                                                                                                                                                                     WashU-Merck EST Project
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                     The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.2%;
Best Local Similarity 100.0%;
Matches 74; Conservative
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                                                                                                                                      Contact: Wilson RK
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BASE COUNT ORIGIN

mRNA

CUS INITION ESSION

RESULT

δλ g

g ò ORGANISM

SOURCE

NID KEYWORDS

REFERENCE AUTHORS JOURNAL

TITLE COMMENT

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Denaturation: 94C 10sec
Annealing: 60C 10sec
Extension: 72C 20sec
                                                                                                             Chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMUT1054 450 bp
Human STS UT1054.
L17757
                                                                                                                                                                                                                                                                                                                                Query Match 1.9%;
Best Local Similarity 82.4%;
Matches 28; Conservative
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230..250
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                          MgC12:
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          Buffer:
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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                                                                                                                            FEATURES
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STS sequence; primer; sequence tagged site. human Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 12 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Canden, NJ 08103.
                                                                                                                                     normalization to a cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopteryg11; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 727259687
                                                                                                                                                                                                                                                                                                                           Score 22; DB 95; Length 267;
Pred. No. 2.15e-04;
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 11; Indels
                                                                                                                                                                                       Minoru Ko (Wayne State University)."
/clone="313003"
/clone_lib="Soares mouse p3NMF19.5"
/dev_starge="19.5" dpc total fetus"
/lab_host="DH10B (amplcillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                             gaagctgctggaaggcgaagagagagtgatttctctgcctctgc 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 ng
each 1 uM
each 200 uM
: 0.05 units/ul
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human STS SHGC-13782 clone pG-6721.
G10922
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Primer B: IGGTGGGGAGTATCAGGTTC
STS size: 98
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taq Polymerase:
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                                                                                                                                                                                                                                                                                                                         Luery Match
Best Local Similarity 75.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR Cycles:
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dNTPs:
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                                                                                                                                                                                                                                                                           mRNA
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KEYWORDS

SOURCE

RESULT

Сp g

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FITELL

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 450)
Gerken,S.C., Matsunani,N., Lawrence,E., Carlson,M., Moore,M., Ballard,L., Melis,R., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Rodriquez,P., Albertsen,H., Lalouel,J.-M. and White,R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer; STS sequence; microsatellite marker; microsatellite
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                          Length 400;
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Pred. No. 2.15e-04;
....matches 6; Indels
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Homo sapiens DNA.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
primer A: TTGGGCTCCTTTCTGGCAAG
Primer B: GGCAAAATGCCTTTGGCATGC
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230..437
/standard_name="STS UT1054"
                                                                                                                                                                             organism="Homo sapiens"
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퓔퓔풭
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complement(308..327)
/map="12"
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complement(418..437)
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2.5
20
20
8.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGIS; T42477; AGIS July 1995.
AGIS; T42477; AGIS July 1995.
Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@lbm.cl.msu.edu. NCBI gi: 933235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                 372 acagagagagtnagnnggagagaaagannnanagataggaataaaagcatgcaaa 426
                                                                                                  W10113;
912844330
29-ARR-1997 (Rel. 51, Last updated, Version 2)
05-MAR-1997 (Rel. 51, Last updated, Version 2)
ma42d03.rl Scares mouse p3NMF19.5 Mus musculus cDNA clone 313349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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   Score 22; DB 48; Length 450;
Pred. No. 2.15e-04;
0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22; DB 77; Length 472
Pred. No. 2.15e-04;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 472 BP; 126 A; 97 C; 100 G; 137 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                   02-FEB-1995 (Rel. 42, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 15)
5740 Arabidopsis thaliana cDNA clone 113K15T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="var columbia"
/note="thale cress"
                                                                                                                                                                       standard; RNA; EST; 472 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="113K15T7"
Best Local Similarity 63.6%;
Matches 35: Concerns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 68.6%;
Matches 35; Conservative
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AT4774
T42477;
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Tel: 314 286 1800
Fax: 314 286 1801
Email: mouseesfewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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mp53f02.rl Soares 2NbMT Mus musculus cDNA clone 572955 5'.
AA117046
                           Uppublished.
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
Mashington University School of Medicinep 4444 Forsts Park Parkway,
Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
Email: mouseest@watson.wustl.edu This clone is available
royalty_free through LLNL; contact the IMAGE Consortium
(info@image.llnl.gov) for further information. Putative full length
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Pred. No. 3.88e-03;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="313349"
/clone_11b="Soares mouse p3NMF19.5"
/dev_stage="19.5 Gpc total fetus"
/lab_host="DH108 (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                   Minoru Ko (Wayne State University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA <1..5105
Sequence 105 BP; 57 A; 13 C; 21 G; 14 T; 0 other;
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WashU-HHMI Mouse EST Project
Washington University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              891 AAAGAAAGTGGGAGCAGAAGACATTGAAAAAAAAAAAA 929
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                   "The WashU-HHMI Mouse EST Project";
                                                                                                                                            read Seq primer: mob.REGA+ET.
Key Location/Qualifiers
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Best Local Similarity 76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Mus musculus
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 Waterston R.;
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JOURNAL
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US-08-915-004-8.rst2

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and Eco RI sites of the modified pT7T3 vector. RNA provide
                                                                                                /clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                /clone="572955"
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Fax: 314 286 1810
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                                                                                                  /note="vector: pT/T3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; [5' rgrraccaarcreaagregeagcegecegegrifitrilitritritritritrit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Confider: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov) for further information, MGI:347603 Pitative full length read vector to vector length is 108 Seq primer: -28MI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubbque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Mortis M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
Waterston R.,
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertębrata; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae;
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0
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18-F¢B-1997 (Rel. 51, Last updated, Version 2)
mp53‡02.rl Soares 2NbMT Mus musculus cDNA clone 572955 5′
                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
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Pred. No. 3.88e-03;
 vector to vector length is 108 seq primer: -28M13 rev2 from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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/clone_lib="Soares 2NbMT"
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                                                                      /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                    /dev_stage="4 weeks"
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                                                                                     /strain="C57BL/6J
                                                                                                                                                                                                                                                                                     /sex="male"
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Best Local Similarity 76.9%;
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by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructedby Bento Soares and M.Fatima Bonaldo."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Rucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,R., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                               Length 107;
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1.8%; Score 21; DB 98; Length 107;
Best Local Similarity 76.9%; Pred. No. 3.88e-03;
Matches 30; Conservative 0; Mismatches 9; Indels
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Sequence 107 BP; 50 A; 16 C; 24 G; 17 T; 0 other;
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Seq primer: -28M13 rev2 from Amersham.
Location/Qualifiers
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Page

BASE COUNT

ORIGIN

mRNA

13

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ACCESSION

WORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygli; Choanata;
Petrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
     G11923
91036742
STS sequence; primer; sequence tagged site.
human STSS derived from random genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Primer A: TGTTTGTAGTTGTTTGTTATTTGGA
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dNTPs: each 4 nM
Taq Polymerase: 0.025 units/ul
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                                                                                                                                                                                                                                                                                                                                                                                          Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer B: AAAGGAGTCAAAATGGGTTTTT
STS size: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denaturation:
Annealing: 56 degrees C
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3
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PCR Profile:
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                                                                                                                                                                                      Hudson, T.
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                                                                            ORGANISM
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ORIGIN
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         ACCESSION
                                                                                                                                                                       REFERENCE
                                                                                                                                                                                        AUTHORS
                                         KEYWORDS
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Eukaryotae; mitochondrial eukaryotes; Catarrhini; Hominidae; Homo.

Fortebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lo (Carken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M., Ballard,L., Melis,R., Robertson,M., Bradley,P., Elsner,T.,
Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R.
Genetic and physical mapping of simple sequence repeat containing sequence tagged sires from the human genome
Submitted by: Utah Center for Human Genome Research University of Utah. Dept. of Human Genetics
Salt Lake City, UT 84112

Salt Lake City, UT 84112

e-mail: sts@corona.med.utah.edu
Primer A: CTACTORGGAGGGGGAGC
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                                                                                                                                                                                                                                                                                                                                                                             PCR primer; STS sequence; microsatellite marker; microsatellite repeat; repeat polymorphism; sequence tagged site. Homo sapiens DNA. Homo sapiens
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                                                                                                                                                                   Gaps
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Pred. No. 3.88e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 48; Length 194;
Pred. No. 3.88e-03;
0; Mismatches 15; Indels
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Gel: Acrylamide 7%, Formamide 32%, Urea 34%
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                                                                                                                                                                                                                            891 AAAGAAAGTGGGAGCAGAAGACATTGAAAAAACAATAAA 929
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                                                                          17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial Denaturation: 94C 300sec
PCR Cycles: 5
Benaturation: 94C 10sec
Annealing: 58C 10sec
Extension: 72C 20sec
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(161..181)
                                                                        24 9
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                                                                                                                                                                                                                                                                                                            HUMUT5145 194 bp
Human STS UT5145.
L17708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION human STS MR4116.
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1.8%;
Best Local Similarity 70.0%;
Matches 35; Conservative
                                                                                                                           Query Match 1.8%;
Best Local Similarity 76.9%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32P-label: A Primer PCR Profile:
                                                                          16 c
                                                                                                                                                                   30; Conservative
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primer_bind
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RESULT 14

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BASE COUNT

STS

ATURES

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Whitehead Institute/MIT Center for Genome Research; Physically Mapped STSs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(134..155)
/map=791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
963_G_6"
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56..155
/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
963_G_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;
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                                                                                                           Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 incitigadatgitaccicatitaaaaaaaacccattitgactccitti 156
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Best Local Similarity 70.8%; Pred. No. 3.88e-03;
Matches 34; Conservative 0; Mismatches 14; Indels
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29..53
/map="923_H_8; 959_F_5; 441.7 cR from top of Chr17 linkage
group"
                                                                                                                  Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Anniota; Mammalia; Theria; Eutheria; Archonta; Primates;

Catarrhini; Hominidae; Homo.

I (bases 1 to 253)

Hudson, T.

Hudson, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
29..253
/map="923_H_8; 959_F_5; 441.7 cR from top of Chr17 linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(235..253)
/map="923_H_8; 959_F_5; 441.7 cR from top of Chrl7 linkage
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                                                        SIS sequence; primer; sequence tagged site. human SISs derived from sequences in dbESI and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prepared with primer pairs derived from 238433 -- dbEST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 38; Length 253; Pred. No. 3.88e-03; 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                      Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
FIL 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    708 ACACAGCTCACAAGAACAGACTTTCCAGCTGCTGAAG 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer A: CATTTGCTTTCATACATACAGTCC Primer B: CACAGTTGTGAAGCCGTGC STS size: 225 PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Tag Polymerse: 0.025 units/ul
Total Vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Best Local Similarity 78.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MgC12: 1.5 mM
KC1: 50 mM
Tris-HCL: 10 mM
pH: 9.3
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                                                                                                                                                                                                                                                                                                Unpublished (1995)
  human STS WI-6406
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TITLE
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                                                        KEYWORDS
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Search completed: Tue Dec 2 16:04:01 1997 Job time: 747 secs.

	(TA)
Release 2.1D John F. C Copyright (c) 1993, 19 Distribution r	Collins, Biocomputing Research Unit. 994, 1995 University of Edinburgh, U.K. rights by IntelliGenetics, Inc.
MPsrch_nn n.a n.a. database	se search, using Smith-Waterman algorithm
Run on: Tue Dec 2 16:04	:23 1997; MasPar time 910.66 Seconds
bular output not generated.	ooo willon cell abaac
Jule: >US-08-915-004- Description: (1-1089) from U Perfect Score: 1089 N.A. Sequence: 1 ATGAACAA Comp: TACTTGTT	915-004-10) from USO8915004.seq ATGAACAAGTTGCTGTGCTGTAAAAATAAGCTGCTTATAA 1089 TACTTGTTCAACGACACGACATTTTATTCGACGAATAT
Scoring table: TABLE default Gap 6	
Nmatch STD : Dbase 0; Query	0 8
Searched: 362067 seqs, 54	49138275 bases x 2
Post-processing: Minimum Match 0	0% 45 summaries
-new3 BCT 2:FUN 3	GEN1 4 GEN2 5
MAM 9:BC 5:BC	11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC 5T2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7 5T9 27:BCT10 28:BCT11 29:GEN1 30:GEN2
2:HT 9:IN 46:M 3:PA	TC1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3 NV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10 AAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 ART 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG LN2 61:PLN3 62:PLN4, 63:PLN5 64:PLN6 65:PLN7
72.PRI3 73.PRI4 74 72.PRI3 73.PRI4 74 79.PRI10 80.PRI11 85.RODI 86.RODZ 87 92.RODB 93.STR 94:: 99.VRL4 100.VRL5 11	LAW 68:PLN10 69:PLN11 70:PR11 71:PR18 78:PR19 R14 74:PR15 75:PR16 76:PR17 77:PR18 78:PR19 PR111 81:PR112 82:PR113 83:PR114 84:PR115 PD2 87:ROD3 88:ROD4 89:ROD5 90:ROD6 91:ROD7 PR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3 98:VRL3 PR15 101:VRL5 102:VRL7 103:VRL9 104:VRL9
3 07:G 13:V	GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV :VRT 114:PHG 115:PLN 116:PR11 117:PR12
ROD 150_	120:UNA
Statistics: Mean 11.131; V	Variance 4.282; scale 2.599
Pred. No. is the number of score greater than or equal and is derived by analysis or	f results predicted by chance to have a all to the score of the result being printed, s of the total score distribution.

SUMMARIES

1	Result No. Sc	core	Query Match	Length	D B	Ð	Descripti	uc	Pred. No.
28 2.6 354 110 0FU9929 OXYTICIDA fallax 57kD 128.7 128.2 1 354 8 0FU9929 OXYTICIDA fallax 57kD 128.2 1 354 8 0FU9929 OXYTICIDA fallax 57kD 128.2 1 354 8 0FU9929 OXYTICIDA fallax 57kD 128.2 1 354 8 0FU9929 OXYTICIDA fallax 57kD 128.2 1 15519 34 1879PID HUMAND NON sequence ** 5 2 1 15519 34 1879PID HUMAND NON sequence ** 5 2 1 15519 34 1879PID HUMAND NON Sequence ** 5 2 1 1374 3 LSRNAGRP L. Stagnalis mRNA for 2 1 13818 1 17 43 LSRNAGRP L. Stagnalis mRNA for 2 1 13819 1 1 1 1 0FU9929 OXYTICIDA fallax 57kD 128.2 1 145100 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9379 OXYTICIDA fallax 57kD 128.2 1 14510 65 SCE9370 OXYTICIDA fallax 57kD 128.2 1 14510 OXYTICIDA fallax 57kD 128.2 1 14510 OXYTICIDA fallax 57kD 128.2 1 14510 OXYTICIDA fallax 57kD 128.2 1 14510 OXYTICIDA fallax 57kD 128.2 1 14510 OXYTICIDA fallax 57kD 128.2 1 14510 OXYTICIDA fallax 57kD 128.2 1 14510 OXYTICIDA fallax 57kD 128.2 1 14510 OXTICIDA OXITICIDA fallax 57kD 128.2 1 14510 OXTICIDA OXITICIDA OXI		30	٠ .	. (1)	57	128278	equenc	from pat	
25 2.9 354 11 07089239 Oxytricina fallax 57kD 24 2.2 354 11 07089239 Oxytricina fallax 57kD 24 2.2 15519 34 110 07089239 Oxytricina fallax 57kD 24 2.2 15519 34 113098239 Oxytricina fallax 57kD 25 3 2.1 155117 HSJIPA, H. sapiens LIPA gene, 2.2 115113 11 HSJIPA, H. sapiens LIPA gene, 3.2 11 1511 54 1517		9 8	٠	C) r	57	128278	edneuc	from paten	.20e-03
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1 (bases I to 354)

Doak, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G. A proposed superfamily of transposase genes: transposon-like
                                                                                   3; Gaps
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1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use tecntrol fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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Doak,T.G., Williams,K., Witherspoon,D.J. and Herrick,G.
Direct Submission
Submitted (11-FBB-1997) Oncological Science, University of Utah, School of Med. Rm5C334, USA, UT 84132, USA
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/note="this is a bulk sequence that was generated from
PCR product that represents many transposon templates"
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13-Mar-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
elements in ciliated protozoa and a common 'D35E' motif
Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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"A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common 'D35E' motif";
proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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Best Local Similarity 30.1%;
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Oncological Science, University of Utah, School of Med. Rm5C334,
USA, UT 84132, USA
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13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera gene, partial
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"A proposed superfamily of transposase genes: transposon-like
elements in ciliated protoca and a common 'D35E' motif";
proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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3 (bases 1 to 354)
Doak, T.G., Williams, R., Witherspoon, D.J. and Herrick, G.
Direct Submission
Submitted (11-FEB-1997) Oncological Science, University of Utah, School of Med. Rm5C334, USA, UT 84132, USA
Location/Qualifiers
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A proposed superfamily of transposaes genes: transposan-like
elements in ciliated protozoa and a common 'D35E' motif
Proc. Natl. Acad. Sci. U.S.A. 91 (3), 942-946 (1994)
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hypotrichs; Stichotrichida; Oxytricha.
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Doak, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G.
                                         Submitted (11-FEB-1997) to the EMBL/GenBank/DDBJ databases.
Oncological Science, University of Utah, School of Med. Rm5C334,
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  Doak T.G., Williams K., Witherspoon D.J., Herrick G.;
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/organism="Homo sapiens"/clone="799F10"
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H.sapiens LIPA gene, exon
X75491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome-"22"
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Aslanidis, C.
                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                 Hunt, A.
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AUTHORS
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MEDLINE
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AUTHORS
                                                                                                                           JOURNAL
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                                                                                                                                                                                         COMMENT
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Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry, University
of Vienna, Waehringerstrasse 17, 1090 Vienna, AUSTRIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-AUG-1992) G. Wiche, Institute of Biochemistry and Molecular Biology, University of Vienna, Dr. Bohrgasse 9, 1030
                                                                                                                                                               rgcdagrgaryhhyhdwargwbgydgwgcyykaayaagcwagmgarwyaswrtrygtaar 158
                                                                                                                                                                                         Murines, Rattus.

1 (bases 1 to 7095)
2aunter, W., Kratz, J., Staunton, J., Feick, P. and Wiche, G.
Identification of two distinct microtubule binding domains on recombinant rat MAP 1B
Eur. J. Cell Biol. 57 (1), 66-74 (1992)
                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
799F10; HTGS phase 1.
                                                                                                                                                                                                                                                                                                                                                                      RRMAP1B5 7095 bp RNA ROD 21-0C1
R.norvegicus mRNA for microtubule associated protein IB.
X60370 X60371 X60550
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                                                                           Score 25; DB 8; Length 354;
Pred. No. 1.33e-01;
38; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.2%; Score 24; DB 92; Length 709
Best Local Similarity 76.1%; Pred. No. 5.89e-01;
Matches | 35; Conservative 0; Mismatches 11; Indels
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               HQYAYKVYPFNYLX"
Sequence 354 BP; 106 A; 42 C; 41 G; 54 T; 111 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAP1B gene; microtubule-associated protein
                                                                                                                                                                                                                                                gawdkcrcgcaaccwvytrrcmtcdgagrtmacdaar 195
                                                                                                                                                                                                                                                                                        CTTTGGTGCCAGGCAAATTGTCTACCAAGACACTAAG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="C6 glioma"
1856 c 1799 g 1316 t
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/dev_stage="adult"
/tissue_type="brain"
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                                                                           Query Match 2.3%;
Best Local Similarity 23.7%;
Matches 23; Conservative
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Rattus norvegicus
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HTG; HTGS_PHASE1.
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TITLE JOURNAL

AUTHORS

REFERENCE

source

TURES

TITLE JOURNAL

REFERENCE

REMARK

AUTHORS

BASE COUNT ORIGIN

DEFINITION

RESULT

g ò ACCESSION

KEYWORDS

SOURCE

ACCESSION

159

Dp

g

694

ORGANISM

KEYWORDS

SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

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with foreign sequence from E.coli, yeast, vector, phage etc. Order of sequence: BT799F10 contig__DD 00052 Length: 992 bp Unfinished sequence: BT799F10 contig__DD 00051 Length: 885 bp Unfinished sequence: BT799F10 contig__DD 00061 Length: 885 bp Unfinished sequence: BT799F10 contig__DD 00185 Length: 885 bp Unfinished sequence: BT799F10 Contig__DD 00185 Length: 885 bp Unfinished sequence: BT799F10 Contig__DD 00963 Length: 958 bp Unfinished sequence: BT799F10 Contig__DD 00968 Length: 958 bp Unfinished sequence: BT799F10 Contig__DD 00968 Length: 958 bp Unfinished sequence: BT799F10 Contig__DD 00166 Length: 958 bp Unfinished sequence: BT799F10 Contig__DD 00165 Length: 13712 bp Unfinished sequence: BT799F10 Contig__DD 02165 Length: 13712 bp Unfinished sequence: BT799F10 Contig__DD 02165 Length: 1371 bp Unfinished sequence: BT799F10 Contig__DD 02224 Length: 1000 bp Unfinished sequence: BT799F10 Contig__DD 02224 Length: 1341 bp Unfinished sequence: BT799F10 Contig__DD 02225 Length: 1341 bp Unfinished sequence: BT799F10 Contig__DD 02225 Length: 1341 bp Unfinished sequence: BT799F10 Contig__DD 02225 Length: 1341 bp Unfinished sequence: BT799F10 Contig__DD 02225 Length: 1341 bp Unfinished sequence: BT799F10 Contig__DD 02224 Length: 1341 bp Unfinished sequence: BT799F10 Contig__DD 02224 Length: 1341 bp Unfinished sequence: BT799F10 Contig__DD 02224 Length: 1367 bp.
                                                                                                                                                                                                                                            Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests. clonerequest@sanger.ac.uk IMPORTANT: This sequence is unfaished and does not necessarily represent the correct sequence. Work on the sequence is in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1851). Aslamidis, C., Klima, H., Lackner, K.J. and Schmitz, G. Genomic organization of the human lysosomal acid lipase gene (LIPA) Genomics 20 (2), 329-331 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * This sequence is unfinished. When sequencing is complete, the sequence data presented in this record will be replaced *by a single finished sequence with the same accession number.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                      Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 115419)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24169 a 28425 c 26764 g 23990 t 12071 others
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NEEDIAFASGLNGGTPDSMLEALPDDLYFTDFVSPFTAAATTS<sup>V</sup>TTKTVKÖTTPATNH
MDDDIAMFDSLATTQPIDIAASNQQNGEIAQLWDFNVDQFNNTPSNSSGSATISAPNS
FTSDIPQYINNSSLGNSVSKSSLFPYNSSTSNSNINQPSINNNSNTNAGSHHSFRIYKL
NNNSSSSAMNITNNNNSNIQHPFLKKSDSIGLSSSNITNSVRKNSLIKPRSSTS
LANNKSRSASSSAMNITNNNNSNIQHPFLKKSDSIGLSSSNITNSVRKNSLIKPRSSTS
LANNKRAASVSSSISMEPSGONKKPLIQCFNCKTFKFPLWRRSPEGNTLCNAGCLFQ
KLHGTMRPLSLKSDVIKKRISKKRAKQTDPNIAQNIPSAPATASTSVTTINAKPIRSR
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FNGASNANLNORNLMARHNNYTGNFRSSRRSSTSSTSSSKSSSRSSVPILERFS
PNGASOFNNNMALMYTTNNYTGNFRSSRRSSTSSTSSSKSSSRSVPILERFS
PNSANGOCHNUMMALMYTTNNYTGNFRSSPRISSANFNSNSPLOONLLSNSFQRO
GMNIPRKMSRNASSRSSFMAAGLOGLHEQOOVDVNSWTNTNSNRGNWASSNSFYRS
ESSNFYSCRPRDIFWTPVDSPSVSRFSSKKHTSLLSOQLONSESNSFISNHKFNNR
LSSDSTSPIKTRADVSAGGKISEDNSTKGSSKESSAIADELDWLKFGI"

3 704 c 530 g 767 t
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/db_xref="PID:g171600"
/translation="MQDDPENSKLYDLLNSHLDVHGRSNEEPRQTGDSRSQSSGNTGE
                                                                                                                                                  YSCGLN3 3021 bp DNA PLN 15-SEP-1990
S.cerevislae nitrogen regulatory protein (GLN3) gene, complete cds.
M35267
                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 3021)
Minehart, P.L. and Magasanik, B.
Sequence and expression of GLN3, a positive nitrogen regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1990)
Draft entry and computer readable [or printed] sequence for [1]
kindly submitted by P.Minehart, 19-JUN-1990.
Author address: P.Minehart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS LSRNAGRP 3177 bp RNA INV 22-JUL-1996 DEFINITION L.stagnalis mRNA for glutamate receptor InvGluR-K1 polypeptide.
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            Gaps
                                                                                                                                                                                                                                                  nitrogen regulatory protein.
S.cerevisiae (strain S288C) DNA.
Saccharomyces cerevisiae
Succharomyces cerevisiae
Eukaryotae; mitochondrial eukaryotes; Fungi; Ascomycota;
Hemlascomycetes; Saccharomycetaceae;
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Best Local Similarity 74.5%; Pred. No. 2.50e+00;
Matches 35; Conservative 0; Mismatches 12; Indels
            9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cp 1038 AAATAACTICIGATACAATITGTACATIGIGAAGCTGTGAAGGAACC 992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..301
/organism="Saccharomyces cerevisiae"
1..140
                                                region"
          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="GLN3"
/note="acidic activation
/db_xref="SGD:L0000710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SGD:L0000710"
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/note="GLN3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cambridge, MA 02139.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="GLN3"
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77 Mass Ave.
          32; Conservative
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Direct Submission
Submitted (02-NOV-1993) C. Aslanidis, Inst for Clinical Chemistry &
Lab. Med., University of Regensburg, 93042 Regensburg, FRG
Location/Qualifiers
1..1851
/organism="Homo sapiens"
/clone_lib="human placenta DNA cloned in lambda FIXII
(strategene)"
(strategene)"
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Submitted (02-NOV-1993) C. Aslanidis, Inst for Clinical Chemistry &
Lab. Med., University of Regensburg, 93042 Regensburg, FRG
Location/Qualifiers
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Aslanidis,C., Klima,H., Lackner,K.J. and Schmitz,G. Genomic organization of the human lysosomal acid lipase gene (LIPA)
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acid cholesteryl ester hydrolase; lipA gene; lysosomal acid lipase.
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Pred. No. 2.50e+00;
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949..1137
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/gene="LIPA"
/EC_number="3.1.1.13"
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Aslanidis, C.
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Best Local Similarity 78.08;
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/ note-"coded for by C. elegans cDNA yk3b5.5; coded for by C. elegans cDNA yk3b5.3; coded for by C. elegans cDNA yk2a5.5; coded for by C. elegans cDNA yk8b4.5; coded for by C. elegans cDNA yk8b4.5; coded for by C. elegans cDNA yk8b4.5; coded for by C. elegans cDNA yk8b4.3; coded for by C. elegans cDNA yk8b4.3; coded for by C. elegans cDNA yk8b4.5; coded for by C. elegans cDNA yk8b62.3; coded for by C. elegans cDNA yk46e2.5
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/evidence=not_experimental
/gene="F55C12.4"
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/gene="F55C12.3"
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/translation="MTSTHWKRLSTLVIGLALVHCARCLPELLKIGGLFGEGDEHTSI
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VDLPVDDTTLFLKMALQEGMIDPYHHYIVTHLDIESIDMEDFRHNYVNLTGFRLVDPS
DPQVKKIIHMEIYEMPOLSLLNTTGYLSLHPHYALMYSORYLLANDERRAFABIL
RPLNASCSTPSQWASGPSILSFLNQIPMEGTGDILLKSGFRIDFKLDIMQLTSKGLV
KGGEWRVSSGINISYHEGQNSCNPFGNKTLVYTSLKESFFLMDRENDSPDEPFEGFCI
DLTKELAKIVGFNFRIELVPDGNYGSNNAEGEWDGWYREIIDRRADLAIAPLITYIR
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NIDTYKRMYAYWKDRPHYMSDSYTEGTAKVKKGNYAFFMENIAIDYGVCRUCDLMQVG
GTLDSKSYGTGLDPMNSPYPAKDLSMALIELLQEAGACH QMLYNKWWKDTGTCTREDTKESK
ANALGYEBVGGIEPLALGALAVIYAIIEFTYKSKENAYEBKGSLCNEMAEBLRFAI
RCTGASKRPKNKFKSRCQDCREGKPHSSHSHHLQEIGPESPPNGIVQLRPTKKSPSAV
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ARFSPYEMYNPHPCNPDIDLVENTFNLSNSFWFTVGTLMQQGSDINPRAVSTRIVGGI
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Submitted (23-MAY-1995) M.G. Darlison, Inst. fuer Zellbiochemie &
Klinische, Neurobiologie, Universitaets-Krankenhaus Eppendorf,
Universitaet Hamburg, Martinistr. 52, 20246 Hamburg, FRG
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                                                                                                                                                                                    ., Amar, M., Harvey, R.J., Bermudez, I., van Minnen, J. and
                                                                                                                                                                                                     Darlison,M.G.
Structure and pharmacological properties of a molluscan
glutamate-gated cation channel and its likely role in feeding
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/db_xref="PID:e183756"
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Caenorhabditis elegans
Eukaryotae; mitcohondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Mollusca;
Gastropoda; Pulmonata; Basommatophora; Lymnaeidae; Lymnaea.
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Pred. No. 2.50e+00;
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/clone_lib="lambdazAPII"
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                                             glutamate receptor .
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Stuhmer, T., Amar, M.,
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Darlison, M.G.
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Best Local Similarity 81.1%;
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RESULT

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ORIGIN

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Rhabditidae, Caenorhabditis.

[Dases 1 (Dases) 10.38586)

Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Bonfield, J., Burton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Coulson, A., Craxton, M., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Kirken, L., Roopra, A.,
Sauders, D., Shownkeen, R., Smaldon, M., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Waughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING COSMID INFORMATION:
The 5' end lies in a gap followed by the cosmid ZK1248;3' cosmid is F59G1, 200 bp overlap. Actual start of this cosmid is at base position 1 of CELF55C12; actual end is at base position.
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KIRMOFEVIRENEMENNEINGIVRSSSTTGMIYDKLANISSRPDNLMDGHQKVRKSLI
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/ ACTION OF THE TRANSLATION OF THE TRANSLA
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Location/Qualifiers
1..38586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(9962..10169,10311..10417,10467..10778,
110830..11285,11330..11492,11141..12262,12310..12831,
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Department of Genetics, Washington University,
Department of Genetics, Washington University,
ST. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRO, England
e-mail: rw@nematcde.wustl.edu and jes@sanger.ac.uk
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Saccharomyces cerevisiae
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Dietrich, F.S.
                                                                                                                                                                                                                           Saccharomyces.
1 (bases 1 to 43100)
Dietrich, F.S.
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                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1994)
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                                                                                                                                 DVSPHPSMRSIDSISKSEERIASRRSSGGSSDOLKOSKVPDNSNDESVETLEETVAKR
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                                                                                                                                                                                                                                                                                     PSMVSQVIYDMKDATVSLRPKRLARRRWWSRKYPIHIRPAHSSSSLVEIDHSSRAKSR
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IADTPSLADELAGGDSSQLLDALREQEICNQKLRVYINGILMRVIERHPEILEIGEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="PID:g1086797"
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Pred. No. 2.50e+00;
0; Mismatches 19; Indels 1; Gaps
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Best Local Similarity 70.6%;
Matches 48; Conservative
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Dietrich,F.S., Mulligan,J., Hennesy,K., Allen,E., Araujo,R.,
Aviles,E., Barno,A., Brennan,T., Carpenter.J., Chen,E.,
Aviles,E., Herno,A., Brennan,M., Guzman,E., Hartzell,G.,
Hunicke-Smith,S., Hyman,R., Kayser,A., Komp,C., Lashkari,D.,
Lew,H., Lin,D., Mosedale,D., Makahara,R., Namath,A., Norgren,R.,
Smogren,T., Smith,V., Taylor,P., Wei,Y., Yelton,M., Botstein,D. and
GLN3 (positive nitrogen regulatory protein); MEI4 (meiosis-specific gene); HOM3 (aspartate kinase); CAJ1 (dnaJ homolog); tRNA-Gln. baker's yeast strain-5288C (AB972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOSLPAIKGTITHSWGDSKVESHVIIINDPASPASNTSEATSSKQFKTPIIGNENTTS
TTSPSNLEPAIKGTRILKKNKGKQQENIDDAEDGSSKKEHHVYKALALAKNRNRQARITS
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EFFYTSLNNKSDEYSVKYTSKPERKANCONDESSENGDGDNDHDDDYDDDDDDDDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLQSSLYETKSESHPPNHPHSQILQTPAKIVITPSVSDAQSQALAITDDDGEDDDDDT
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EAESYMFSDEAPSIESGPANAKSTRGIYSQSNKNIIRDGKPNYSFSLKRNNSDDETEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLRGGSKNREVSPFSSVSSSFRSTHSFNGKLTINQGAKELAPMKNKIELTNKTVTFFN
SNNWNTYDCNSLSRKTSSQMRDSKYQNHNVGQNVEPSSVLSPQHQISNGLDGKCNDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STPSQMNYDSIPPPAKHSPGFESFHRLANKTSKLFKKTSNSNLNSHLASTPTTSTNQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISNSFVLONPPIKNTGPPPPLPPPLFPSSSTSSFSRHDNESEYTAYKKTSPAKDFNRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSAIKASLTGTTGSTKPTVKSFSDIFNVDDSASDAESDSGTGGNNSNGLVSNDSERQV
                                                                                                                                                                                                                                                                                                                                        The sequence of S. cerevisiae cosmids 9379, 9581, and lambda clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neighboring Sequence:
The 5' end of this sequence overlays with GenBank Accession Number
018778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete sequence of Saccharomyces cerevisiae chromosome V Unpublished (1994)
                                                                                                                                              Eukaryotae, mitochondrial eukaryotes; Fungi, Ascomycota;
Hemiascomycetes; Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted by: Stanford DNA Sequence & Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto, CA 94304, USA e-mail: dietrich@genome.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Saccharomyces cerevisiae"
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177..41762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Saccharomyces cerevisiae"
/strain="S288c (AB972)"
/chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Saccharomyces cerevisiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/product="Yer033p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            855 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="S288C (AB972)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(297..3527)
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CDS

CDS

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LANFKRAASVSSISNMEPSGQNKKPLIQCFNCKTFKTPLWRRSPEGNTLCNACGLFO
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PNSANSQQFNMNLMTTNNVSAGNSVASSPRIISSANFNSNSPLQONLLSNSFQRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMNIPRRKMSRNASYSSSFWAASLQQLHEQQQVDVNSNTNTNSNRQNWNSSNSVSTNS
RSSNFVSQKPNFDIFNTPVDSPSVSRPSSRKSHTSLLSQQLQNSESNSFISNHKFNNR
LSSDSTSPIKYEADVSAGGKISEDNSTKGSSKESSAIADELDMLKFGI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLLFFSVLLGADYNRGVKGLGKNKSLQLAQCEDPNFSMEFYDJFKDFNLEDLTSESLR
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                                                                                                                                                                                        AMVISGLMSVGISYCSGWCVRVTSSTTYSMVGALNKLPIALAGLVFFDAPKNFLSFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTSDIPQYNHGSLGNSVSKSSLFPYNSSTSNSNINOPSINNNSNTNAQSHHSFNIYKL
QNNNSSSSAMNITNNNNSNNSNIQHPFLKKSDSIGLSSSNTTNSVRKNSLIKPMSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKELLSLNVEFLLVFDGVMKPSFKRKFNHEQNATTCDDEKEYYSSWEQHVKNHEVYGN
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RLPOKNNLDEFLRKHTSPIKSIGKVGESRKEILEPVRKRLFVDTDEDTSLEEIPAPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTTVDEHSDNDDDSLIFVDEITNSQSVLDSSPGKRIRDLTQDEQVDVWKDVIEISPIK
KSRTTNAEKNPPESGLKSRSSITINARLQGTKMLPPNLTAPRLEREHSSVLDQLVTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIDESDNIGKGNMRITEEKIMNIDGGKFQIPCFKIRYTTFLPNIPISSQSPLKRSNSP
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                                                                                                                                                                                                                                                                                                                                         /note="YER040w; positive nitrogen regulatory protein; contains putative zinc finger (GABA type) domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-1997
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Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
111224; HTGS phase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145750)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to DNA repair protein Rad2p from S. cerevisiae, Swissprot Accession Number P07276" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 12932 aaaaaacctctgatacaatgtttcaattgtaaaaactttcaagacacc 12978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 65; Length 4310
Pred. No. 2.50e+00;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cp 1038 AAATAACTICIGATACAATITGTACATIGIGAAGCIGIGAAGGAACC 992
                                                                                                                                                                                                                               IFLGFLSGLLYAVAKQKK IQQQKVLAATLEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="YER041w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 2.1%;
Local Similarity 74.5%;
les 35; Conservative
                                                                                                                                                                                                                                                                                                 /gene="GLN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
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TASPDISFHYEGVYSQHSQDQLDLTKRALEFPDKYS SNISQDFGFWRGQLGFTPQSG
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VVSHDFRLLDKIAQDIFVVENKTATRWDGSILQYKNKLLAKNVVL"
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LSSFANAWFIDDNESNVRSALSMGMGHVIHLIEDYQYESENIVTKDHKNKQQFSILKD
ILEIPLIMDVEVYRPSSIAIKEMEELEEEGGEAVNWSNQQINVQSS"
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NLCTIFPVNKMLKFLMYFYSDDDNDDVREFFLKAFICLILDRKVFNAMESDHRLCFKV
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                                                                                                                                                                                                                       /db_xref="PID:g603267"
/translation="MDAFSLKKDNRKKFQDKQKLKRKHATPSDRKYRLLNRQKEEKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAQHELKRIEDDVEKTILEDGPESELLEPLYERMDSLDPDFESRAAIILIGLGFNKK
TILKKTKDMSGGWKMRVALAKALFVKPTLLLLDDPTAHLDLEACVWLEEYLKRFDRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="PID:g603270"
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EYGLSVKGLIKNKQIDDVLQYNTFIDDSLPLQDYLKPDWKLRELLINLKKKKLGKFDK
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NEDEEIVKTPRKLVNYVPLKIFNLGDSFDDTITTTVAKLQDLKKEILDSPRSNKSIVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to hypothetical protein F42A10.1 from Caenorhabditis elegans, GenBank Accession Number U10414; contains motifs typical of ABC transporter proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s.
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VISPNLPTTITPTNSFTKPTPEFSNDYSLSPIQETPSSVQSSPKRA"
                                                                                                                                                    /evidence=not_experimental
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                                                                      /qene="YER034w"
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vith foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished sequence: dJIIIJ24 Contig_ID: 00116 Length: 13962 bp Unfinished sequence: dJIIIJ24 Contig_ID: 00234 Length: 13962 bp Unfinished sequence: dJIIIJ24 Contig_ID: 00331 Length: 10666 bp Unfinished sequence: dJIIIJ24 Contig_ID: 00331 Length: 794 bp Unfinished sequence: dJIIIJ24 Contig_ID: 00031 Length: 5939 bp Unfinished sequence: dJIIIJ24 Contig_ID: 00704 Length: 4939 bp Unfinished sequence: dJIIIJ24 Contig_ID: 01917 Length: 4359 bp Unfinished sequence: dJIIIJ24 Contig_ID: 01904 Length: 5518 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02681 Length: 6356 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02681 Length: 6358 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02147 Length: 5188 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02187 Length: 5188 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02187 Length: 5188 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02187 Length: 5188 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02187 Length: 5188 bp Unfinished sequence: dJIIIJ24 Contig_ID: 02255 Length: 21019 bp.
           Direct Submission
Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CBI0 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and
                                                                                                                                                                                                                                                                         the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *** WARNING: Phase 1 High Throughout Genome Sequence ***
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36917 a 31170 c 31921 g 33145 t 12597 others
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TITLE
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                                                                                                                                                                             COMMENT
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Search completed: Tue Dec 2 16:35:46 1997 Job time: 1883 secs.

Db 82692 gaaacaacaaaacaaagaccaagat 82716

Query Match 2.1%; Best Local Similarity 96.0%; Matches 24; Conservative

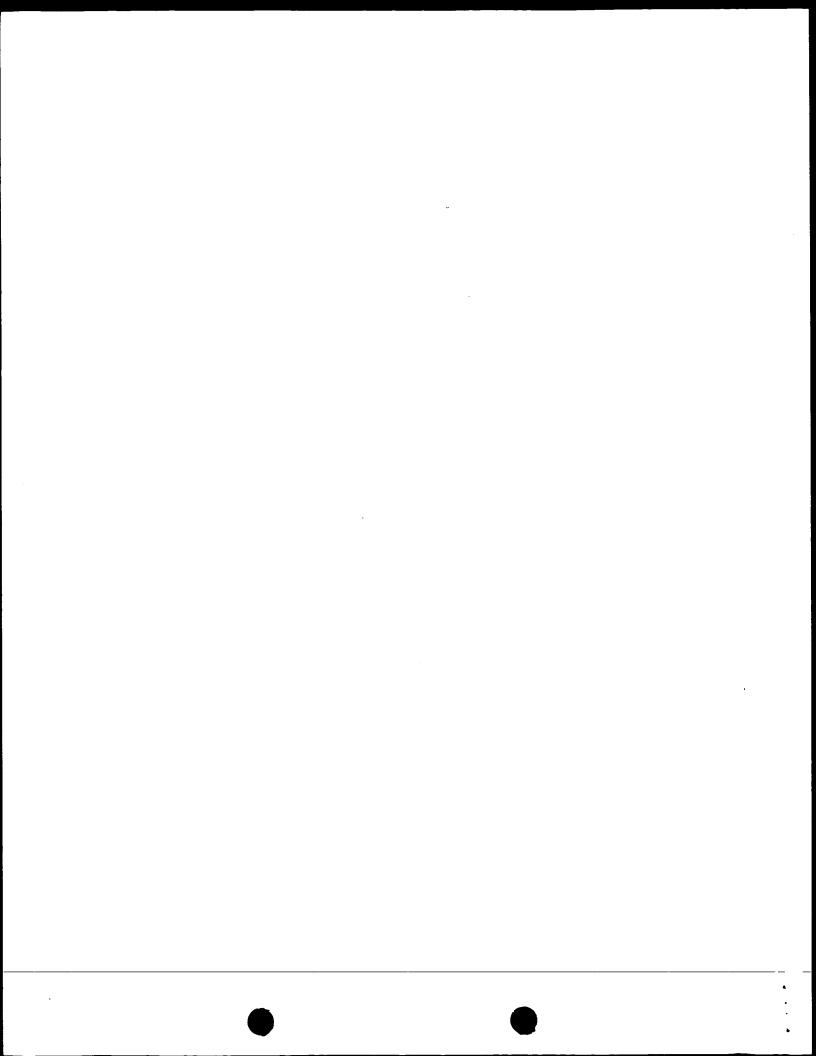
ö

Gaps

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Length 145750;

Score 23; DB 33; Length 145 Pred. No. 2.50e+00; 0; Mismatches 1; Indels



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Run on:

Tue Dec 2 17:04:56 1997; MasPar time 59.59 Seconds 814.423 Million cell updates/sec ular output not generated.

......AGATAGTTGTGACAGTTTAG 465 >US-08-915-004-12 (1-465) from US08915004.seq 465 Description: Perfect Score: Sednence tle:

TABLE default Gap Scoring table:

142080 seqs, 52183452 bases x 2 Searched:

Dbase 0; Query 0

STD

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

n-geneseq28 l:part1 2.part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28

Mean 8.278; Variance 4.498; scale 1.841 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

_	% Query					
Score Match Length DB	Lengt	a ;	8	ID	Description	Pred. No.
465 100.0 465	465		28	T36688	Osteoclastogenesis in	0.00e+00
94.0 1	10190		27	T33183	Fragment of human OCI	0.00e+00
400 86.0 1173	1173		28	T35475	Human tumour necrosis	2.10e-285
399 85.8 438	438		28	T36689	Osteoclastogenesis in	1.28e-284
85.6	432		27	T33176	Mutated OCIF, OCIF-CC	7.76e-284
85.6	564		27	T33180	Mutated OCIF, OCIF-CB	7.76e-284
85.6	594 2	"	7	T33175	Mutated OCIF, OCIF-CD	7.76e-284
85.6	819 2	. 4	7	T33174	Mutated OCIF, OCIF-CD	7.76e-284
398 85.6 966	996	٠.	2	T33179	Mutated OCIF, OCIF-CS	7.76e-284
85.6	981		27	T33170	Mutated OCIF, OCIF-DD	7.76e-284
85.6	984		27	T33171	Mutated OCIF, OCIF-DD	7.76e-284
	1056		27	T33173		7.76e-284
85.6	1080		27	T33169	Mutated OCIF, OCIF-DC	7.76e-284
	1182		27	T33178		7.76e-284
398 85.6 1200	1200		27	T33172	Mutated OCIF, OCIF-CL	7.76e-284

Query Match 100.0%; Score 465; DB 28; Length 465; Best Local Similarity 100.0%; Pred. No. 0.00e+00;

.76e-2	7.76e-284	.87e-28	.87e-28	.87e-28	.87e-2	.03e-21	.35e-21	.30e-16	17e-14	66e-11	.50e-1	48e-1	.30e-1	.61e-1	.23e-1	.23e-1	.11e-0	Ħ	.11e-0	.32e-0	.55e-0	.31e-	.31e-	.31e-	4.6	.46e-0	4	.83e-0	.53e-0
Osteoclastogenesis in	Mutated OCIF, OCIF-C2	Mutated OCIF, OCIF-C1	Mutated OCIF, OCIF-C2	OCIF, OCIF	ed OCIF, OCIF	Mutated OCIF, OCIF-CC		ted OCIF,	ted OCIF, OCIF-	Mutated OCIF, OCIF-DC	atriuretic	Human Natriuretic Pep	substituted	gonucleotide	Oligonucleotide probe	substitute	eric DNA sec	c DNA sequenc	C DNA	Generic DNA sequence	ic DNA :	Generic DNA sequence	Generic DNA sequence	Generic DNA sequence	ic DNA s	Generic DNA sequence	ic DNA s	Generic DNA sequence	Generic DNA sequence
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ALIGNMENTS

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for bone resorption control, esp. treatment of osteoporosis Claim 22; Page 74; 183pp; Japanese.
This sequence encodes full length osteoclastogenesis inhibitory factor (OCIF) 4. The OCIF of the invention has a molecular weight by SDS-PAGE Of ND under reducing conditions and 120 ND under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                         22-APR-1997 (first entry)
Osteoclastogenesis inhibitory factor 4 coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                    DNA encoding osteoclastogenesis inhibitory factor protein - useful
                                                                                                                                                                                                                                                                                            Morinaga T;
                                                                                                                                                                                                                                                                                                          Yasuda H
                                                                                                                                                                                                         29-AGC-1996.
20-FEB-1995; JP-05374.
20-FEB-1995; JP-057508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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                                                                                                                       Location/Qualifiers 1..63
T
T36688 standard; DNA; 465 BP.
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                                                                                            osteoporosis; ss.
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W09626217-A1.
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mat_peptide
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                                                                                                                                                                                                                                    CACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA 360
                                                                                                                                                                                                                                                                           361 CATAGGAGCTGCCTCCTGGATTTGGAGTGGTGCAAGCTGGTACGTGTCAATGTGCAGCA 420
                                                                                                                                                                                                                                                                                                                                                                          23-APR-1997 (first entry)
Fragment of human OCIF genomic DNA-2.
Osteqclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                    121 |TGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACC 180
                                                                                                                                                                                                                                                         cataggagetgecetectggatttggagtggtgeaagetggtaegtgtcaatgtgeagea 420
                  1 atgaacaagttgctgtgctgctcgctcgtgtttctggacatctccattaagtggaccacc 60
                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - useful
                                                                                                                                                                                              CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
gawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
96-402320/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding osteoclastogenesis inhibitory factor protein-
bone resorption control, esp. treatment of osteoporosis
0; Indels
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/note= "encodes residues 252 to 380 of OCIF, see R99925"
WO9656217-Al.
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"encodes residues -11 to 112 of OCIF, see R99925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "encodes residues 113 to 176 of OCIF, see R99925'
                                                                                                                                                                                                                                                                                                aaattaattaggatcatgcaaagtcagatagttgtgacagtttag 465
                                                                                                                                                                                                                                                                                                                 AAATTAATTAGGATCATGCAAAGTCAGATAGTTGTGACAGTTTAG 465
0; Mismatches
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
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                                                                                                                                                                                                                                                                                                                                                         T33183 standard; DNA; 10190 BP.
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 465; Conservative
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Claim 91; Page 152-161; 183pp; Japanese.

The sequences given in T33182-83 represent fragment of the genomic DNA encoding the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 50 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cteettetagittetggaeateteeattaagitggaeeaceaggaaaegitteeteeaaa 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 gtaccttcattatgacgaagaaacctctcatcagctgttgtgtgacaaatgtcctcctgg 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 CTCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACCCAGGAAACGTTTCCTCCAAA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Tumour necrosis facor; INF; receptor; INF-beta; ligand; tumour; differentiation; immune response; autoimmune disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 tacctacctaaaacaactgtacagcaaagtggaagaccgtgtgcgcccttgccctga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 CAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCCACAACCGCGTGTGCGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 GTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCGG
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                                                                                                                                                                                                                                                                                                                                                   3187 T;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 437; DB 27; Length 10190; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                   1899 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   septic shock; graft-versus-host; apoptosis; ss.
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                                                                                                                                                                                                                                                                                                                                                3184 A;
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I35475 standard; cDNA; 1173 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                               94.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 99.1%;
nes 441; Conservative
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15-MAR-1995; U03216,
15-MAR-1995; WO-U03216,
29-MAR-1995; ZA-002587,
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/*tag= a
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New human tumour necrosis factor receptor - used to develop prods.

To treating e.g. tumours, infection, auto:immune disease, graft
rejection, cytotoxicity or inflammation

Claim 1, Fig 1; 59pp: English

Claim 2, Fig 1; 59pp: English

Claim 3, Fig 1; 59pp: English

Claim 4, Fig 1; 59pp: English

Claim 5, Fig 1; 59pp: English

Claim 6, Fig 1; 59pp: English

Claim 7, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

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Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 59pp: English

Claim 1, Fig 1; 5pp: English

Claim 1, Fig
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Osteoclastogenesis inhibitory factor 5 coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTGCGCCCCTTGCCCTGACCACTACTACACAGACAGCTGGCACACCCGTGACGAGTGT 240
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I Similarity 99.5%; Pred. No. 2.10e-285;
402; Conservative 0; Mismatches 2;
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F, Mochizuki S,
Ueda M, Yano K,
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21-JUL-1995; JP-207508.
21-JUL-1995; JP-207508.
CSNOW SNOW BRAND MILK PROD CO LTIGOTO W, Higashio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Uev PSDB; W99930.
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T36689 standard; DNA; 438 BP.
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20-FEB-1996; J00374.
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claim 24; Page 76; 183pp; Japanese.
This sequence encodes full length osteoclastogenesis inhibitory factor (OCIF) 5. The OCIF of the invention has a molecular weight by SDS-PAGE 06 60 KD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                           121 tgtgacaaatgtcctcctggtacctacctaaaacaacatgtacagcaaagtggaagac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300
                                                                                                                                                                                                                                                                                                                                                             gtgtgcgccccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GIGIGGGCCCCTIGCCCTGACCACTACTACAGAGACAGCTGGCACACCAGTGACGAGTGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 caggaaacgittcciccaaagtaccitcattatgacgaagaaaccictcatcagcigitg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1997 (first entry)
Mutated OCIF, OCIF-CCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                        1 atgaacaagttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 72; Page -; 183pp; Japanese. This sequence encodes a mutated version of the full length
                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa
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                                                                                                                                                                                                    Score 399; DB 28; Length 438; Pred. No. 1.28e-284;
                                                                                                                                                                         94 T;
                                                                                                                                                                                                                                          1; Indels
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Ueda M, Yano K,
                                                                                                                                                                         110 G;
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                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                       117 C;
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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Nakagawa N, Shima N, Tsuda E,
WPI; 96-402320/40.
                                                                                                                                                                     117 A;
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T33176 standard; DNA; 432 BP.
                                                                                                                                                                                                     Match 85.8%;
Local Similarity 99.8%;
(es 400; Conservative
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WO9626217-A1.
                                                                                                                                                                       438 BP;
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osteo clastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CCR4 in which amino acids 123-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the protein sequence and the wild type OCIF CDNA sequence given in T36685. Sequence 432 BP; 116 A; 117 C; 106 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300
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Mutated OCIF, OCIF-CBsp, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                                                                                        3; Indels 0; Gaps
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                                                                                                                                                                                                                                           ch 85.6%; Score 398; DB 27; Length 432; 1 Similarity 99.3%; Pred. No. 7.76e-284; 401; Conservative 0; Mismatches 3; Indels
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20-FEB-1995; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
P-PSDB: R99950.
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W09626217-A1.
                                                                                                                                                                                                                                                                  Best Local Similarity
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DNA ehcoding osteoclastogenesis inhibitory factor protein – useful for bone resorption control, esp. treatment of osteoporosis Claim 84; Page 149-150; 183pp; Japanese.

Morinaga T; Yasuda H;

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and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 degr. Cor 30 mins at 56 degr. C, and is lost after 10 mins at 90 degr. C. OCIF is useful in the control of bone resorption and therefore
This sequence encodes a mutated version of the full length osteoolastogenesis inhibitory factor (OOIF) of the invention. This sequence encodes OOIF-CBSp in which amino acids 167-380 of the mature protein have been deleted. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed ont
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Mutated OCIF, OCIF-CDD1, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                              61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
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                                                                                                                                                                                             in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                     1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAACAAGTTGCTGTGCTGCTCGTCGTGTTTTCTGGACCATCTCCATTAAGTGGACCACC 60
                                                                                                                                                                                                                                                                                                               3; Indels 0; Gaps
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                                                                                                                                                                                                                                                                          Score 398; DB 27; Length 564; Pred. No. 7.76e-284;
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F, Mochizuki S,
Ueda M, Yano K,
                                                                                                                                                                                                                                     132 G;
                                                                                                                                                                                                                                                                                                                 0; Mismatches
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20-FEB-1996, J00374.
20-FEB-1995, JP-054977.
21-JUL-1995, JP-207508.
(SNOW) SNOWW BRAND MILK RODD CO LIT GOLO M, Highshio K, Kobayashi F, Nakagawa N, Shima N, Tsuda E, Ue
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T33175 standard; DNA; 594 BP.
                                                                                                                                                                                                                                     159 A;
                                                                                                                                                                                                                                                                        ch 85.6%;
1 Similarity 99.3%;
401; Conservative
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W09626217-A1.
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P-PSDB; R99945.
                                                                                                                                                                                                                                   564 BP;
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Synthetic.
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This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutated version of the invention. This sequence encodes OCIF-CDD1 in which amino acids 177-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the protein sequence and the wild type OCIF cDNA sequence given in T35685. Sequence 594 BP; 176 A; 152 C; 136 G; 130 T;
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                           1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
                                                                                                                                                                                                                                                                                    / Match 85.6%; Score 398; DB 27; Length 594; Local Similarity 99.3%; Pred. No. 7.76e-284; les 401; Conservative 0; Mismatches 3; Indels
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20-AuG-1996, J00374.
20-FEB-1995, JP-054977.
21-JUL-1995, JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
The Higashio K, Kobayashi F, Mochizuki S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
Claim 69; Page -; 183pp; Japanese.
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T33174 standard; DNA; 819 BP
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22-APR-1997 (first entry)
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for bone resorption control, esp. treatment of osteoporosis Claim 66. Page 145; 183p; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DD2 in which amino acids 252.380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Pred. No. 7.76e-284;
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20-FEB-1996. 100374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
5NOW ) SNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S, Makagawa N, Shima N, Tsuda E, Ueda M, Yano K,
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P-PSDB; R99949.
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          This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CSph in which amino acids 280-380 of the mature protein have been deleted and replaced by Ser-Leu-Asp. These amino acid changes have been caused by the introduction of a restriction site.

The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing productions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 966 BP; 301 A; 228 C; 226 G; 211 T;
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Mutaqed OCIF, OCIF-DDD1, coding sequence.
Osteqclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UL1-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI: 96-402320/40.
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Pred. No. 7.76e-284;
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81; Page 149; 183pp; Japanese.
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Claim 54, Page 141-142; 183pp; Japanese.

This sequence encodes a mutated version of the full length octeoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD1 in which amino acids 178-252 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 981 BP; 312 A; 238 C; 218 G; 213 T;
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg
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Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.6%; Score 398; DB 27; Length 981;
larity 99.3%; Pred. No. 7.76e-284;
Conservative 0; Mismatches 3; Indels (
for bone resorption control, esp. treatment of osteoporosis
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a M, Yano K,
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29-AUG-1996; J00374,

20-FEB-1996; JP-054977.

20-FEB-1995; JP-07508.

21-JUL-1995; JP-207508.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

GOLO M, Higashio K, Kobayashi F, Mochizuk

GOLO M, Shima N, Tsuda E, Ueda M, Yan
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T33171 standard; DNA; 984 BP.
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/product= OCIF-DDD2
WO9626217-A1.
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401; Conser
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Matches 4
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This sequence encodes mutated version of the full length of steoldstogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD2 in which amino acids 253-356 of the mature protein have been deleted. The OCIF of the invention has a molecular non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. of 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                              T33173 standard; DNA; 1056 BP.
T33173;
22-APR-1937 (first entry)
Mutated OCIF, OCIF-CC, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                   121 tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtgtgcgcccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240
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                                                                                                                                                                                                                                                                                              1 atgaacaacttgctgctgctgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
                                                                                                                                                                                                                         Score 398; DB 27; Length 984;
Pred. No. 7.76e-284;
0; Mismatches 3; Indels
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Claim 63; Page 144-145; 183pp; Japanese.
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20-FEB-1995; JP-0374.
20-FEB-1995; JP-207508.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
 Claim 57; Page 142-143; 183pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 1..63
                                                                                                                                                                                                                           85.68;
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                                                                                                                                                                                                                                                            401; Conservative
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                                                                                                                                                                                                                                          Local Similarity
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W09626217-A1.
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This sequence encodes a mutated version of the full length obsteoclassis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CC in which maino acids 311-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. ociF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
                                                                                                                                                                                                                                                                               1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                                                                                                                                                                              1 ATGAACAAGTIGCIGIGCIGCICGIGITITCIGGACAICTCCATTAAGTGGACCACC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                      tgtgacaaatgtcctcctggtacctacctaaaacaactgtacagcaaagtggaagacc
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Yasuda H;
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Ueda M, Yano K,
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85.6%; Score 398; DB 27; L
Best Local Similarity 99.3%; Pred. No. 7.76e-284;
Matches 401; Conservative 0; Mismatches 3;
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29-AUG-1996.
20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Moc
Nakagawa N, Shima N, Tsuda E, Ueda M,
WPI: 96-402320/40.
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I33169 standard; DNA; 1080 BP.
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osteo clastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CR4 in which amino acids 123-164 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under nor-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption and therefore in the treatment and sequence 1080 BP. 345 M. 256 C. 244 G. 235 T;
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Osteqclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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This sequence encodes a must add version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
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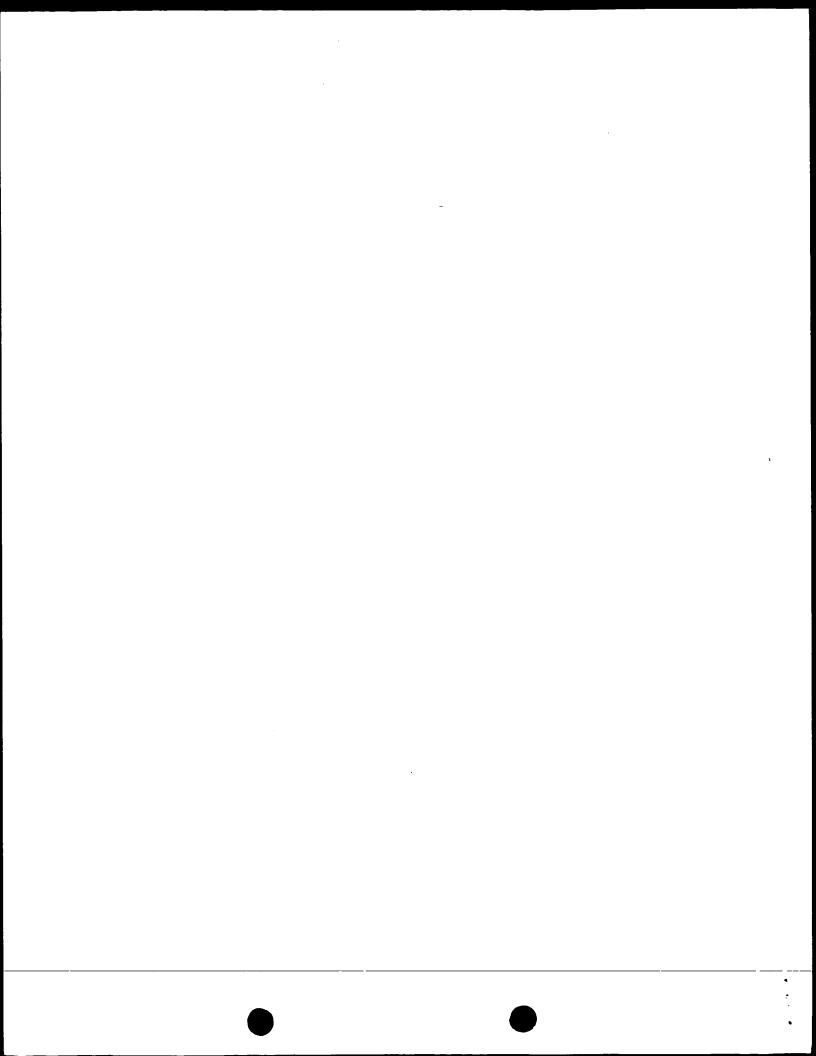
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sequence encodes OCIF-CBst in which Gln371 is substituted with Leu and amino acids 373-380 of the mature protein have been deleted. These amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing on conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the provention of disorders of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-CL, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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This sequence encodes a mutated version of the full length
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
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osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CL in which amino acids 379-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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74506.s1 Soares ret 1.03e-04
74606.s1 Stratagene 1.03e-04
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   179:EST179
184:EST184
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175:EST175 176:EST176 177:EST177 180:EST180 181:EST181 182:EST182 185:EST182 185:EST182 195:EST197 192:EST197 195:EST197
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Location/Qualifiers
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Best Local Similarity 71.2%;
Matches 37; Conservative
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                                                                                                                           Contact: Wilson RK
                                                                          Unpublished (1995)
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JOURNAL
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AUTHORS
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SOURCE
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                                                                                                                                          double-stranded cons was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library went constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured actic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deuterostomia; Chordata, Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Anniota; Mammalia; Theria; Eutheria; Archonua; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 344)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Riffini,L., Rohliging,T., Scares,M., Tan,F., Tar,F., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zn46h08.rl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550527 5'.
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                  vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsitel=Not I Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a Not I oligo(dr) primer [8]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stops: 313 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1996
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 300)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
human clone=163472 library=Soares adult brain N2b4HB55Y
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Pred. No. 1.72e-07; 
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 gcaccacttcccctnactactnctacncacacagct 152
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/clone="163472"
a 116 c 86 g 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                         midbrain, pons and medulla.
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WashU-Merck EST Project
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Best Local Similarity 77.8%;
Matches 28; Conservative
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygil; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 258.
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1 (bases 1 to 453)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Wash U-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N21157 453 bp mRNA EST 19-DEC yx47d01.s1 Homo sapiens cDNA clone 264865 3' similar to SP:TCPB_MOUSE P80314 T-COMPLEX PROTEIN 1, BETA SUBUNIT ;
                                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 GTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Stratagene HeLa cell s3 937216" /sex="female"
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                                                                                                                                                             WashU-Merck EST Project
Washington University School of Medicine
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\bar{\rm EST}({\rm expressed}\ {\rm sequence\ tag}) . Organ shoot (8 days old) cDNA to Oryza sativa (strain Nipponbare, ) Green shoot (8 days old) cDNA to
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55c10 Human retina cDNA randomly primed sublibrary Homo sapiens
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                                                                     Gaps
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 cgggtgcantnacggcaaccaggtgctcaaggagctngaggaggccaagaaggngt 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 CGAGTGTCTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGT 289
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Liliopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 493)
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                                                                                                                                  Length 493;
                    Length 472;
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Pred. No. 4.46e-06;
0; Mismatches 19; Indels
                                                               0; Mismatches 16; Indels
                                                                                                            365 gaaacagttgctgnaagctaccttgagtttgcccaagaaacccttnatnag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice Genome Research Program
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Nipponbare"
/dev_stage="Green shoot (8 days old)"
147 c 150 g 93 t 5 otl
                      Score 22; DB 57; ] Pred. No. 4.46e-06;
                                                                                                                                                                                                                      RICS15559A 493 bp mRNA
Rice cDNA, partial sequence (S15559_1A).
D48963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from shoot
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-Feb-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity 66.1%;
Matches 37; Conservative
                    Query Match
Best Local Similarity 68.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phone: 0298-38-7441
Fax : 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ibaraki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 472)
Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,
McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M.,
Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                           High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand.
Location/Qualifiers
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Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                            WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 453;
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T42477
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Pred. No. 4.46e-06;
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97 c 100 g
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                                                                                                                                                                         Email: est@watson.wustl.edu
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Best Local Similarity 77.5%;
Matches 31; Conservative
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66
                                             Contact: Wilson RK
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Fax: 517-353-9168
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human clone=73829 library=Stratagene fetal spleen (#937205)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primcr=Mi3RPl Rsitel=ECORI Rsite2=xhoi Pooled fetal spleens. Cloned
unidirectionally. Primer: Oligo df. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: 5' adaptor sequence: 5'-GAATTCGGCACGAG-3'; 3'
adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTTTTT".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 325)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Washiymerck Ext project

Washiymerck Ext project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read.
                                                                                                                                                                                                                                                                                                                                 08-FEB-1995
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TGESTzy27b03.rl Toxoplasma gondii cDNA clone tgzy27b03.rl 5'
similar to SW:EF1A_PLAFK Q00080 ELONGATION FACTOR 1-ALPHA ;.
N61165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                             2047904 325 bp mRNA EST 08-FE yb42d03.r1 Homo sapiens cDNA clone 73829 5' similar to 95:03910_rnal Human (HUMAN).
T54964
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                                                                                                                                                             Length 300;
   Score 21; DB 48; Length 300;
Pred. No. 1.03e-04;
6; Mismatches 15; Indels
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Query Match
Best Local Similarity 58.8%;
Matches 30; Conservative
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Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Maraneith, A., Takeda, S., Matanabe, T., Takahashi, E. I., Hirai, Y., Unpublished (003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (library: Clontech human aorta polyA+ mRNA (#6572))
CDNA to mRNA.
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/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
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Best Local Similarity 73.9%; Pred. No. 4.46e-06;
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                    Fax: 410 614 0827
Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
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Seg primer: GGGTAAAAAGCAAAAGAATT.
Location/Qualifiers
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FORWARD: CITITGAGCAAGITCAGCCIGGITAAGI
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Tsutomu Fujiwara
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Human aorta cDNA 5'-end GEN-213B09.
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Otsuka Pharmaceutical Co., Ltd
463-10 kagasuno Kawauchi-cho
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 383) Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Rudaa, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fmail: est@watson.wustl.edu
High quality sequence stops: 268
Source: IMAGE Conscrium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                          Score 21; DB 5; Length 376; Pred. No. 1.03e-04;
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yp23h05.s1 Homo sapiens cDNA clone 188313 3'.
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1 (bases 1 to 376)
1 (hases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Source: David Sibley, Washington University Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ajioka,J.A., Aslett,M.A., Dietrich,N., Dubuque,T., Kucaba,T., Marta,M., Sibley,L.D., Wan,K.L. and Waterston,R.A. WashH-Merck Toxoplasma EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                            Eukaryotae; mitochondrial eukaryotes; eukaryote crown group;
Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystida;
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 gtttcgttggtgataaacatggtggagaagtccaccaacatgagc 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 GTTTCCTGGGTGGTCCACTTAATGGAGATGTCCAGAACACGGGC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                          WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 99; 1 Pred. No. 1.03e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Toxoplasma gondii"
/clone="tgzy27b03.rl"
/strain="RH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: toxo@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity 73.3%;
                                                                                    Toxoplasma.
1 (bases 1 to 371)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..>371
                                                                                                                                                                                                                                                                                                    Contact: Marra M
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DEFINITION

RESULT

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ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Gaps

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6; Indels

Length 383;

DEFINITION

RESULT

ACCESSION

KEYWORDS

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FERENCE UTHORS TITLE JOURNAL

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/tissue_type="retina"
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WashU-Merck EST Project
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                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                               AA021559 447 bp mRNA EST 08-AUG-1996
ze69b06.s1 Soares retina N2b4HR Homo sapiens cDNA clone 364211 3'.
AA021559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High qality sequence stops: 304
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                          01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
yc50c04.rl Homo sapiens cDNA clone 84102 5' similar to gb:J03910_rnal Human (HUMAN);.
                                                                                                                         human clone=84102 library=Stratagene liver (#937224)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 others
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Pred. No. 1.03e-04;
0; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 GIGCGATIGCACTCCTGCTTGACGTACTGCAGCTCCT 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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WashU-Merck EST Project
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105 c
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Best Local Similarity 78.4%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST
Unpublished (1995)
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BASE COUNT

ORIGIN

FEATURES

DEFINITION

RESULT

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ACCESSION

KEYWORDS

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

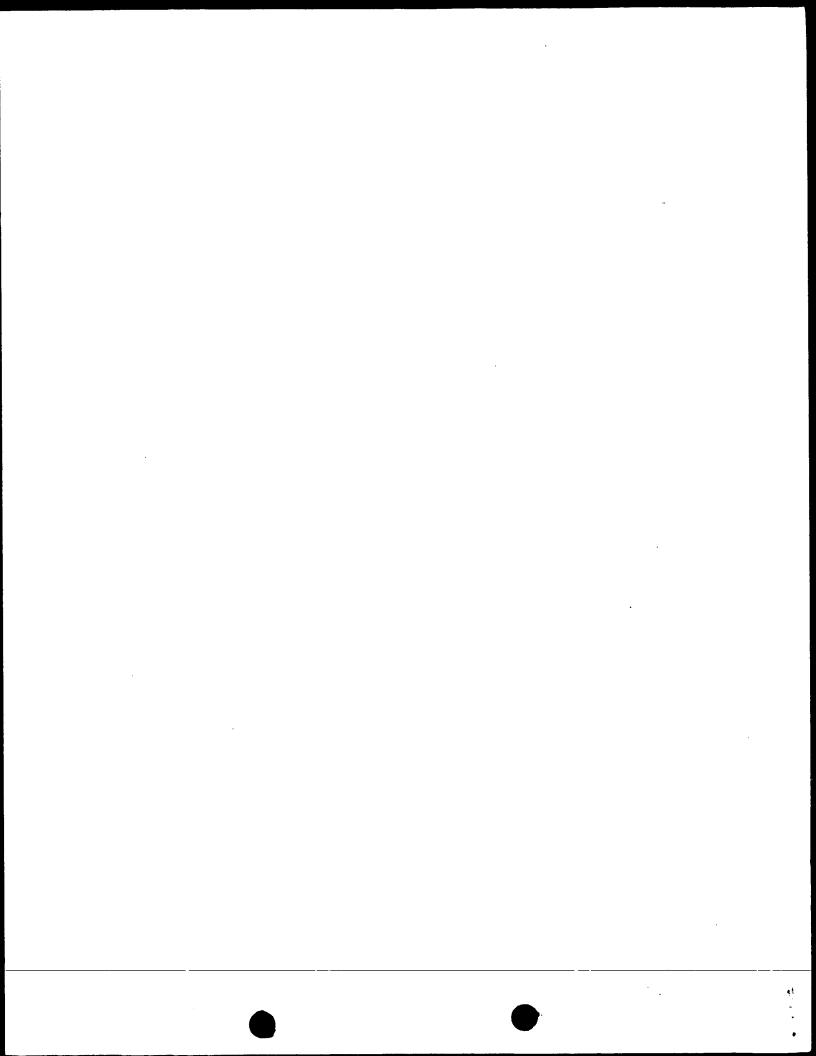
COMMENT

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AA011021 447 bp mRNA EST 29-NOV-1996 234001.s1 Soares retina N2b4HR Homo sapiens cDNA clone 360864 37. g1472048
                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 417.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 603 Std Error: 0.00
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="55 year old"
/lab_bost="HH10B (ampicillin resistant)"
complement(<1..447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares retina N2b4HR"
/sex="male"
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20-C1-1390
2014405.s1 Strategene Helm cell s3 937216 Homo sapiens CDNA clone 550281 3' similar to SW:NIZM_BOVIN Q02369 NADH-UBIQUINONE AAA098806
91644777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4644 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 423.
Location/Qualifiers
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotzei mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 491)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lenon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Wasterston, R., Williamson, A., Wohldmann, P.; and Wilson, R. Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1996
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                 High quality sequence stop: 415.
Location/Qualifiers
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Seq primer: mob.REGA+ET
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WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 bp
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JOURNAL
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epithelioid carcinoma cells grown to semi-confluency without induction. Average insert size: 1.5 kb; Uni-ZAP XR Vector. -5' adaptor sequence: 5' GAATICGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTITITITITITITITI 3'" /clone="550281"
Xhol; Cloned unidirectionally. Primer: Oligo dT. HeLa
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                                                                                                                     /clone_lib="Stratagene HeLa cell s3 937216"
/sex="female"
                                                                                                                                                                                                                                                                                             Score 21; DB 183; Length 491;
Pred. No. 1.03e-04;
0; Mismatches 5; Indels C
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.hes 5; Indels
                                                                                                                                                               /dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
complement(<1..>491)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: Tue Dec 2 17:11:26 1997
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Best Local Similarity 83.9%;
Matches 26; Conservative
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Match Length DB

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1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204

7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210

13:EST211 14:EST212 15:EST213 16:EST214 17:EST215

18:EST212 19:EST217 20:EST218 21:EST214 21:EST215

23:EST212 24:EST227 25:EST223 25:EST224 27:EST225

28:EST226 29:EST227 30:EST228 31:EST229 32:EST236

33:EST226 40:EST23 36:EST23 36:EST23 37:EST230

33:EST24 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
                                                                                                                                            - n.a. database search, using Smith-Waterman algorithm
                                                                    Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variance 1.771; scale 5.717
                                                                                                                                                                                                                                                                                                                                                                                                                                                       359085 seqs, 137405154 bases x 2
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(1-465) from US08915004.seq
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TACTTGTTCAACGACACGAC.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

Result

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AA203500 874 bp mRNA EST 24-JAN-1997 ax58h07.rl Soares fetal liver spleen INFLS S1 Homo sapiens CDNA clone 446749 5' similar to contains element MSR1 repetitive element
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Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
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KEYWORDS
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standard; DNA; STS; 204 BP
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//clone='446749"
//clone=lib="Soares fetal liver spleen INFLS SI"
                                                                                                                                                                                              ö
                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28N13 rev2 from Amersham
High quality sequence stop: 307.
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Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bidg., E. Lansing, Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn6tbm.cl.msu.edu. NCBI gi: 933235

Key
                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Fax: 314 286 1810
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Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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              Washington University School of Medicine
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12-MAR-1997 (Rel. 51, Last updated, Version 15)
5740 Arabidopsis thaliana cDNA clone 113K15T7.
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WashU-Merck EST Project
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Zq16e09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 629896 3' similar to SW:MAPB_HUMAN P46821 MICROTUBULE-ASSOCIATED PROTEIN 1B. ;
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: poly1 not found
Seq primer: -41ml3 fwd. Er from Amersham.
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Hillier, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Wasterston, R., Williamson, A., Wohldmann, P., and Wilson, R., Unpublished (1995)
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                   Sequence 472 BP; 126 A; 97 C; 100 G; 137 T; 12 other;
                                                                                                                                           Score 22; DB 77; Pred. No. 3.31e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 24; Dred. No. 7.41e-05;
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                       /strain="var columbia"
/note="thale cress"
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/clone="113K15T7"
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                                                                                                                                Local Similarity 68.68;
les 35; Conservation
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Best Local Similarity 71.7%;
Matches 33; Conservative
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Homo sapiens (tissue library: LANL flow sorted chromosome 5 library
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Grady.D.L., Robinson,D.L., Gersh,M., Nickerson,E., McPherson,J., Wasmuth,J.J., Overhauser,J., Deaven,L.L. and Moyzis, R.K.
The generation and regional localization of 303 new chromosome 5 sequence-tagged sites
Genomics 32 (1), 91-96 (1996)
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/tissue_lib="LANL flow sorted chromosome 5 library in
M13mp18"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 12; Indels
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Best Local Similarity 72.7%; Pred. No. 1.47e-03;
Matches 32; Conservative 0; Mismatches 12; Indels
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/evidence=experimental
/note="for primer B"
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/note="5qP"
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/evidence=experimental
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Human chromosome 5 LANL STS 200
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                                    Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
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/tissue_llb="LANL flow sorted chromosome 5 library in
M13mpl8"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
Grady, D.L.
Chromosome 5 Project
                                                                                                                                                                              Grady D.L., Robinson D.L., Gersh M., Nickerson E., McPherson J., Wasmuth J.J., Overhauser J., Deaven L.L., Moyzis R.K.; "The generation and regional localization of 303 new chromosome Sequence-tagged sites"; Genomics 32:91-96(1996).
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                                                                                             Homo sapiens (human)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo
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BP; 53 A; 47 C; 38 G; 66 T; 0 other;
                             24-JAN-1996 (Rel. 46, Created)
18-MAR-1997 (Rel. 51, Last updated, Version 3)
Human chromosome 5 LANL STS 200.
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/note="5qp"
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/evidence=experimental
/note="for primer B"
a 47 c 38 g (
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/evidence=EXPERIMENTAL
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/evidence=EXPERIMENTAL
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/evidence-experimental
/note-"for primer A"
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/note-"vector: lambda2apII; Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. Full length cDNA was prepared by long-range RT-PCR from mRNA from L2 larvae of the human filarial nematode parasite Brugia malayi using nematode spliced leader (SL, 5'end) and oligo-d(T) (3' end
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/tissue_lib="LANL flow sorted chromosome 5 library in M13mp18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/brugia/L2S/MBL2SJ8A6T3.html Seq primer: T3.
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Secermentea, Spiruria, Spirurida, Filarioidea; Onchocercidae;
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q1870959
09-MAR-1997 (Rel. 51, Created)
09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2S$J8A6T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ8A6
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                                                                                                                                                                                                                                                                                                                        0; Mismatches 12; Indels
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61 A; 47 C; 56 G; 70 T; 1 other;
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172.197
/evidence=experimental
/note="for primer B"
/note="for primer B"
                                                                           complement(2..26)
/evidence=experimental
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                                                         /chromosome="5"
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
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                                                                               primer_bind
                                                                                                                                                                         primer_bind
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/note="vector: lambdaZapII; Site_1: Eco R I (5' end):
Site_2: Xho I (3' end): Brugia malayi is a lymphatic
filarial nematode parasite of humans. Full length cDN was
prepared by long-range RT-PCR from mRNA from L2 larvae of
the human filarial nematode parasite Brugia malayi using
nematode spliced leader (SL, 5'end) and oligo-d(T) (3'
end) primers. The library had an unamplified titre of -1 x
10E6 per ml and -95% of clones have inserts (mean length
900 bp). The library is available from The Filarial
Genome Project Resource Center: context Dr. S.A. Williams,
Clark Science Center, Smith College, Northampton, MA 01063
USA phone +1 413 583 3826 fax +1 413 585 3786 email
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University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
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Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M., Baron, L. and
                                               Gaps
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Secemnentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
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MBL28J8A6T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ8A6 5'
AA241654
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Fax: +44 131 670 5450
Email: mark.blaxter/ed.ac.uk
Email: trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/L2S/MBL2SJ8A6T3.html
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Score 20; DB 79; Length 235
Pred. No. 1.47e-03;
0; Mismatches 6; Indels
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Pred. No. 1.47e-03;
0; Mismatches 6;
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/sex="mixed"
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/strain="TRS Labs"
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Best Local Similarity 81.3%;
Matches 26; Conservative
  Match 4.3%;
Local Similarity 81.3%;
les 26; Conservative
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/otte-Total And Angeles (1) Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. Full length cDNA was prepared by long-range RT-PCR from mRNA from L2 larvae of the human filarial nematode parasite Brugia malayi using nematode spliced leader (SL, 5'end) and oligo-d(T) (3' end) primers. The library had an unamplified titre of 1 x 10E6 per ml and -95% of clones have inserts (mean length -900 bp). The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email
                                                                                                                                                                            Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
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/lab_host="E. coli XL1-Blue MRF-"
                                                                                                                                                                                                                                                                                                                                                                    Fax: +44 131 670 5450
Email: mark.blaxterefed.ac.uk
The Ail trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/L2S/MBL2SJ0H3T3.html
           Genes expressed in adult female Brugia malayi
Unpublished (1996)
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/strain="TRS Labs"
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/clone_lib="JHU96SL-BmL2"
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Matches 26; Conservative
                                                                                                                                             Contact: Blaxter ML
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Jones, S.J
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/dev_stage="mosquito derived, second stage larvae (L2)"
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Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L. and
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Secernentea, Spiruria, Spirurida, Filarioidea, Onchocercidae,
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МВL2S20H3T3 JHU965L-BmL2 Brugia malayi cDNA clone L2SJ0H3 5′
g1870877
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Location/Qualifiers
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
                                                          AA241559;
91870877
09-MAR-1997 (Rel. 51, Created)
09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2SJOH3T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJOH3 5'
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Sequence 308 BP; 93 A; 65 C; 70 G; 80 T; 0 other;
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Local Similarity 81.3%; Pred. No. 1.47e-03;
Nes 26; Conservative 0; Mismatches 6:
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/strain="TRS Labs"
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                               standard; RNA; EST; 308 BP
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Newman T., deBruijn F.J., Green P., Keegstra K., Kende H., McIntosh L., Ohlrogge J., Raikhel N., Somerville S., Thomashow M., Retzel E., Somerville C.; "Grees galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Physiol. 106:1241-1255(1994).
Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan
                                                                                                                                                                                                                                            Eukaryotae, mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
28-SEP-1996 (Rel. 49, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 5)
26232 Lambda-PRLZ Arabidopsis thaliana cDNA clone 88F5T7.
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DEFINITION ACCESSION

ORGANISM

KEYWORDS SOURCE

NID

REFERENCE AUTHORS

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/organism="Arabidopsis thaliana"
/strain="var columbia"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal quantitie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA inserts were directionally cloned with Sal-Notarms using oligo dT prime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence can be viewed at http://www.sanger.ac.uk/brugia/L2S/MBL2SJ9D7T3.html This is the full sequence of the cDNA clone. The polyA tail has been clipped and is excluded from this sequence Seq primer: T3.

Key Location/Qualifiers
State University MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu Seq primer: T7. Economical Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common 
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
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09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2SJ9D7T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ9D7 5′
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/note="Vector: lambdaZapII; Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filatial nematode parasite of humans. Full length cDNB was prepared by long-range RT-PCR from mRNA from L2 larvae of the human filatial nematode parasite Brugia malayi using nematode spliced leader (SL, 5'end) and oligo-d(T) (3' end) primers. The library had an unamplified titre of -1 x 10E6 per ml and -95% of clones have inserts (mean length -900 bp). The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 S85 3826 fax +1 413 S85 3786 email
primers. The library had an unamplified titre of ~1 x 10E6 pper ml and ~95% of clones have inserts (mean length ~900 bp). The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA genome@smith.smith.edu."
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The ABI trace of this sequence can be viewed at
http://www.senger.ac.uk/brugia/L2S/MBL2SJ9D7T3.html This is the
full sequence of the cDNA clone. The polyA tail has been clipped
and is excluded from this sequence
                                                                                                                                                                                                                                          /dev_stage="mosquito derived, second stage larvae (L2)"
/lab_host="E. coli XL1-Blue MRF-"
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MBL2S29D7T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ9D7 5'.
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
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Sequence 383 BP; 116 A; 67 C; 78 G; 120 T; 2 other;
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Pred. No. 1.47e-03;
0; Mismatches 6;
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/strain="TRS Labs"
                                                                                                                                                                                             /clone_lib="JHU96SL-BmL2"
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llarity 81.3%; E
Conservative
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Fax: +44 131 670 5450
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/clone_lib="JHU96SL-BmL2"

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/Organism="Brugia malayi"
/Strain="TRS Labs"
/Strain="TRS Labs"
/Note-"Vector: lambdaspII: Site_1: Eco R I (5' end);
Site_2: Xho I (3' end); Brugia malayi is a lymphatic
filarial nematode parasite of humans. Full length cDNA was
prepared by long-range RT-PCR from mRNA from L2 larvae of
the human filarial nematode parasite Brugia malayi using
nematode spliced leader (SL, 5'end) and oligo-d(I) (3' end
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/sex="mixed"
/dev_stage="mosquito derived, second stage larvae (L2)"
/lab_host="E. coli XL1-Blue MRF-"
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/lab_host="E. coli XLI-Blue MRF-"
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Key
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Secernentea; Spiruria; Spirurida; Filarioidea; Onchocercidae;
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09-MAR-1997 (Rel. 51, Last updated, Version 1)
MBL2SJ0E3T3 JHU96SL-BmL2 Brugia malayi cDNA clone L2SJ0E3 5'.
                                                                                                                                                                     Score 20; DB 67; Length 383;
Pred. No. 1.47e-03;
0; Mismatches 6; Indels
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4.3%; Score 20; DB 79; Length 387;
Best Local Similarity 81.3%; Pred. No. 1.47e-03;
Matches 26; Conservative 0; Mismatches 6; Indels
                                                                                                                       2 others
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BP; 121 A; 65 C; 78 G; 123 T; 0 other;
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Unpublished.
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                                                                                                                                                                                                                                                                        401 GTACGTGTCAATGTGCAGCAAATTAATTAGG 432
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Best Local Similarity 81.3%;
Matches 26; Conservative
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401 GTACGTGTCAATGTGCAGCAAAATTAATTAGG 432
137 gtacgtatcaatggtcagcaaagcaatcagg 168
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completed: Tue Dec 2 17:14:28 1997 ne : 160 secs. Search com

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31.8ECT1 9.BCT2 20.BCT3 21.BCT4 22.BCT5 23.BCT6 24.BCT7 25.BCT8 26.BCT9 27.BCT10 28.BCT11 29.GEN1 30.GEN2 31.ECT3 32.HTG1 33.HTG2 34.HTG3 35.HNV1 36.HNV2 37.INV3 38.INV4 39.INV5 40.INV6 41.INV7 42.INV1 46.HNAM1 47.HNAM2 48.HNAM1 42.INV9 44.INV10 45.INV1 46.HNAM1 47.HNAM2 48.HNAM3 49.VRT1 50.VRT2 51.VRT3 52.YRT4 53.PAT1 54.PAT2 55.PAT3 56.PAT4 57.PAT5 58.PHG 59.PAN1 60.PAN2 61.PAN3 62.PAN4 63.PAN5 64.PAN6 65.PAN7 66.PAN8 67.PAN9 68.PAN1 69.PAN1 69.PAN1 77.PR18 78.PR19 72.PR13 73.PR14 74.PR15 75.PR16 76.PR17 77.PR18 78.PR19 72.PR13 73.PR14 74.PR15 75.PR16 76.PR17 77.PR18 78.PR15 93.ROD1 86.ROD2 87.ROD3 88.ROD4 89.ROD5 90.ROD5 91.ROD7 92.ROD8 93.STR 94.SYN 95.UNA 96.VRL1 97.VRL2 98.VRL3 99.VRL3 100.VRL5 101.VRL6 102.VRL7 103.VRL8 104.VRL9
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1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV
9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC
                                                                                                              n.a. - n.a. database search, using Smith-Waterman algorithm
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.
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(1-438) from US08915004.seq
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TACTTGTTCAACGACACGAC.
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Perfect Score:
N.A. Sequence:
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SUMMARIES

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annx 12648 ann Clno 18802 ctrtrepacy 9463

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387 caaggccctgaaggagggcaagtcggtggacaagcccatctacaaccacgtgtccg 442
                                                                                                                                                                                                                                         /dev_stage="adult"
/tissue_type="brain"
/cell_type="C6 glioma"
a 1856 c 1799 g 131
                                                                                                                                                                                                                                 /strain="Sprague-Dawley
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Best Local Similarity 76.1%;
Matches 35; Conservative
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Local Similarity 69.6%;
nes 39; Conservative
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              Wiche, G.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                 [ (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                              asgtsssnggtdgnrsgadsygssktamtsrnrtgktannavdsrnmgdasvgsdknt 157
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| Leases 1 to 7095)
| Zauner, M., Kratz, J., Staunton, J., Feick, P. and Wiche, G. Identification of two distinct microtubule binding domains on recombinant rat MAP 18
| Eliz. J. Cell Biol. 57 (1), 66-74 (1992)
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    Score 28; DB 57; Length 215;
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                                     55; Mismatches 55; Indels
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                     Pred. No. 7.95e-05;
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Sequence 5 from patent US 5569830.
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Best Local Similarity 17.0%;
Matches 23: Constants
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Best Local Similarity 12.8%;
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Rattus norvegicus
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YDALAPEADRYDLMYNGVKALKEGKSVDKPTYNHVSGLIDAPEKISSPPILVIEGLHP
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KLTCSFPGIKMFYGPDTWXGQEVSVLEMDGOFDKLEELIYVESHLSNTSAKFYGEITG
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/db_xref="PID:9167432"
/translation="MAFTMRAPAPRATAQSRVTANRARRSLVVRADKDKTVV1GLAAD
Direct Submission
Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry, University
of Vienna, Wachringerstrasse 17, 1090 Vienna, AUSTRIA
revised by [3]
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Chlamydomonas reinhardtii
Eukaryotae; mitochondiial eukaryotes; Viridiplantae; Chlorophyta;
Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
I (bases I to 1245)
Roesler, K.R. and Ogren, W.L.
Chlamydomonas reinhardtii phosphoribulokinase: Sequence,
purification and kinetics
Plant Physiol. 39, 188-193 (1990)
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                                                                                                                          Wiche, G.
Direct Submission
Submitted (07-AUG-1992) G. Wiche, Institute of Biochemistry and Molecular Biology, University of Vienna, Dr. Bohrgasse 9, 1030
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C.reinhardtii phosphoribuloKinase mRNA, complete cds.
M36123
g167431
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Pred. No. 6.05e-02;
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/codon_start=1
/product="phosphoribulokinase"
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/b_xref-"PD: 9479084"
/db_xref-"SWISS-PROT: P36425"
/translation-"MSIPFSNTHYRIPOGFGNLLEGLTREILREOPDNIPAFAAAYFE
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                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-3AN-1993) O'Rand M. G., University of North Carolina at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel Hill, North Carolina, USA, 27599-7090
revised by [3] MAT
3 (bases I to 1256)
O'Rand,M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-APR-1994) O'Rand M. G., University of North Carolina
at Chapel Hill, Cell Biology & Anatomy, 210A Taylor Hall, Chapel
Hill, North Carolina, USA, 27599-7090
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/note="alternate 5'untranslated region for 1.1 KB mRNA"
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Oryctolagus cuniculus

Bukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;

Bukaryotae, mitochondrial eukaryotes; Metazoa; Chordata;

(bases 1 to 1256)

Richardson, R.T., Yamasaki, N. and O'Rand, M.G.

Sequence of a rabbit sperm zona pellucida binding protein and Doalization during the acrosome reaction

Doalization during the acrosome reaction
                                                                                   02-MAR-1995
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Pred. No. 1.31e+00;
0; Mismatches 17; Indels
                                                                                     MAM
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/strain="New Zealand white"
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/tissue_type="testis"
/cell_type="spermatogenic"
/clone_lib="Rabset"
/clone="SR-16R-16"
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                                                                       O.cuniculus SP17 gene.
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2 (bases 1 to 1256)
O'Rand,M.G.
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Best Local Similarity 69.6%;
Matches 39; Conservative
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-1991
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1 (bases I to 1505)
Lewis, M., Tartaglia, L.A., Lee, A.L., Bennett, G.L., Rice, G.C., Wong, G.H.W., Chen, E.Y. and Goeddel, D.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS MUSMINFR2 1505 bp mRNA ROD 18-APR-1
DEFINITION Mouse tumor necrosis factor receptor 2 mRNA, complete cds.
ACCESSION M60469
                                                                                                                                                                                                                                                                                                                                            /gene="murine tumour necrosis factor receptor 2"
/note="Thr to Ile"
replace(489,"t")
/gene="murine tumour necrosis factor receptor 2"
/note="silent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="murine tumour necrosis factor receptor 2"
/note="Phe to Ile"
replace(921,"c")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Thr to Cys"
replace(1317, "g")
/gene="murine tumour necrosis factor receptor 2"
                                                                                                                                                                                                                                                       /gene="murine tumour necrosis factor receptor 2"
/note="Ser to Thr"
replace(278,"t")
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/note="Ser to Phe"
replace(1047,"t")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(1173, "a")
/gene="murine tumour necrosis factor receptor
/note="silent"
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/gene="murine tumour necrosis factor receptor
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Pred. No. 1.31e+00;
0; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(1143,"t")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace(802, "a")
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                                                                                                                                                                                                                            replace(260, "c")
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417 c 3
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Best Local Similarity 64.1%;
Matches 50; Conservative
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                                                                                                                                                                                                 FDQIAVKVA
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Powell,E.E., Wicker,L.S., Peterson,L.B. and Todd,J.A.
Allelic variation of the type 2 tumor necrosis factor receptor gene
95178848
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//codon_start=1
//Lonsolation="Indiagold"
//translation="Indiagold"
//translation
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Nuffield Dept of Surgery, The John Radcliffe Hospital, Oxford, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Powell, E.E., Wicker, L.S., Peterson, L.B. and Todd, J.A.
Amino acid variation in the tumor Necrosis factor receptor 2 is
linked to autoimmune diabetes in NOD mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toagatgtgctgtgctaagtgtcctcctggccaatatgtgaaacatttctgcaacaagac 167
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                                                                                                                                           /gene="murine tumour necrosis factor receptor 2"
/note="silent"
/replace="t"
1173
                                                                                                                                                                                                                                                                                                                                                                                                            /gene="murine tumour necrosis factor receptor 2"
/note="Thr to Cys"
/replace="g"
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/note="silent"
                                 /gene="murine tumour necrosis factor receptor 2"
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                                                                   /note="silent"
/replace="t"
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/replace="a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae; Mus.
1 (bases 1 to 1388)
Powell, E.E.
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DEFINITION

ACCESSION

ORGANISM

KEYWORDS SOURCE

SASE COUNT

ORIGIN

108

168

δý g δy source

FEATURES

CDS

AUTHORS TITLE

JOURNAL REFERENCE

TITLE

RENCE JTHORS REFERENCE AUTHORS

JOURNAL MEDLINE

TITLE

JOURNAL

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/db_xref="PID: g199828"
/translation="MapaalwyalveElQLwarGHTVPAQVVLTPYKPEPGYECQISQ
FYDRKAGMCCAKCPPGQYVKHFCKTKSDTVCABCASAWTCHSCSCGT
DOVEIRACTKQONNYCACEAGRYCALKTHGSGSCRCCMRLSKCGPGFGVASSRAPMGN
VLCKACAPGTFSDTTSSTDVCRPHRICSILAIPGNASTDAVCAPESPTLSAIPRTLYV
SOPEPTRSQPLDOEPGPSQTPSILTSILAIPGSYRKGEISLPIGILAIPGTSUCAL
IGLVNCIILVQRKKRECLCRDAKVPHYPDRSGDAVGLEQQHLITTAAPSSSSSSES
SASAGDRRAPFGGHPQARVWAEAQGFOEARASSRISDSSHGSHGTHVNVTCIVNVCSS
SHISSQCSQASATVGDPDARVBARSASRISDSSHGSHGTHVNVTCIVNVCSS
SHISSQCSQASATVGDPDARVBARSASRISDSSHGSHGTHVNVTCIVNVCSS
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/db_xref="PID:g202095"
/translation="MAPAALWVALVFELQLWATGHTVPAQVVUTPXKPEPGYECQISQ
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
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Goodwin,R.G., Anderson,D.M., Jerzy,R., Davis,T., Brannan,C.I.,
Copeland,N.G., Jenkins,N.A. and Smith,C.A.
Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor
Mol. Cell. Biol. 11, 3020-3026 (1991)
  Cloning and expression of cDNAs for two distinct murine necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSTNFR1 3796 bp mRNA ROD 01-AUG-1991
Murine tumor necrosis factor I receptor (TNFR-1) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 tcagatgtgctgtgctaagtgtcctcctggccaatatgtgaaacatttctgcaacaagac 252
                    factor receptors demonstrate one receptor is species specific
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                               /product="murine tumor necrosis factor receptor 2"
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Pred. No. 1.31e+00;
0; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor necrosis factor receptor.
Mus musculus lymphoid cDNA to mRNA.
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/cell_line="7B9"
/cell_type="helper T-cell"
                                                                                                                               /organism="Mus musculus"
41..106
/codon_start=1
41..1465
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/map="Chromosome 4"
                                                                                        Location/Qualifiers
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SACHNOIIILOVRKKRESCLQRDAKVPHYPDEKSQDAVGLEQOHLLTTAPSSSSSLES
SASAGDRRAPPGGHPQARVMAEAQGPQEARASSRISDSSHGSHGTHVNVTCIVNVCSS
SDHSSQCSSQASATVGDPDARDSASPKDEQVPFSQEECPSQSPCETTETLQSHERPLP
LGVPDMGMKPSQAGWPDQIAVKVA"
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VORFINLINGGGSERRSCFWKLIRHLDRVDSILLTHIGDDDLFPGINSMLQRKIABLEBE
RSQGSTSNSDWMKNLISLGVVFLAVPENLKDPEPNIKMRRSIEEACFTLQYLNKLS
MKPEPLERSVGNTIEPVILFOKMGVGKLEMYVLNPVRSSKEMQYFMOQMTGINKDRAE
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                       IDQVEIRACTKOONRVCACEAGRYCALKTHSGSCROCMRLSKCGPGFGVASSRAPNGN
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Submitted (09-JAN-1990) Cowan N.J., Dept. of Biochemistry, New York
University Medical Center, 550 First Avenue, New York, NY 10016
2 (bases I to 7620)
Noble, M., Lewis, S.A. and Cowan, N.J.
The microtubule binding domain of microtubule-associated protein
MAPIB contains a repeated sequence motif unrelated to that of MAP2
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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MOUSE MAPIB mRNA for MAPIB microtubule-associated protein.
X51396
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MAP1B gene; microtubule-associated protein.
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                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 90;
Pred. No. 1.31e+00;
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/db_xref="PID:953000"
/db_xref="SWISS-PROT:P14873"
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/dev_stage="5 day old"
/tissue_type="brain"
/clone_lib="lambda GEM"
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/gene="TNFR-1"
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Matches 50; Conservative
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TTRTPEVSGYTYEKTERSRRLLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSPPES
ESYSYETSTKTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTTEKKSPSEARQ
EVTKTSQVEKTPKVESKEKVLVKKDKPVKTESKPSVTEKEVSSKEEQSPVKAEVAEKQ
                                                                                                    KKEIKKEERKELKKEVKKETPLKDAKKEVKKEEKKEVKKEEKEPKKEIKKISKDIKKS
                                                                                                                                                                                                        AATTAAVVAAAGIAASGPVKELEAERSLMSSPEDLTKDFEELKAEEIDVAKDIKPQLE
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XKHMDPPPAPAQDRSPSPRHPDVSMVDPDALAVDQNLGKAVKKDLKEKTKTKKRGTKT
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SKNVDVEFFKRVRSSYYVVSGNDPAREEPSRAVLDALLEGKAQWGSNMQYTLIPTHDS
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Human microtubule-associated protein 1B (MAPIB) gene, complete cds.
                                                  ATESKPKVTKDKVVKKEIKTKLEEKKEEKPKKEVVKKEDKTPLKKDEKPRKEEVKKE:
                                                                                                                                                           TPQSDTKKPSALKPKVAKKEESTKKEPLAAGKLKDKGKVKVIKKEGKTTEAAATAVG
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1 (bases 1 to 9416)
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/product="microtubule-associated protein 1B"
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/product="microtubule-associated protein 1B"
/db_xref="PID:9473431"
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Pred. No. 1.31e+00;
0; Mismatches 12; Indels
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Unpublished (1993)
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166..>7629
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Best Local Similarity 73.9%;
Matches 34; Conservative
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Homo sapiens
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ORIGIN
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Tobases 1 to 17013)
Bugert, P. and Geider, K.
Molecular analysis of the ams operon required for exopolysaccharide synthesis of Erwina amylovora
Mol. Microbiol. 15 (5), 917-933 (1995)
                                                                                                                                                                                                                                                                                                                                                            KSSTPLSEAKKPAALKPKVPKKEESVKKDSVAAGKPKEKGKIKVIKKEGKAAEAVAAA
VGTGATTAAVMAAAGIAAIGPAKELEAERSLMSSPEDLTKDFEELKAEEVDYTKDIKD
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EDEEGAKAEADAYIERKESYASGDRAEEDMOEAIEKGEAEOSEERAEAEAE
EEETSPEKMEADAYIKAVVDKAAEAGGEEQYGFLTTPTKQLGAQSPGREPASSIHDE
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ILPEMEGLSEFTEYLSESVEVPSPFDILEPPTSGGFLKLSKPCCYIFPGGRGDSALFA
                                                                                                                            QSQGSTINSDWMKNLISPDLGVVFLNVPENLKNPEPNIKMKRSIEEACFTLQYLNKLS
                                                                                                                                                                                                 FILPNGQEVDLPISYLTSVSSLIVWHPANPAEKIIRVLFPGNSTQYNILEGLEKLKHL
DFLKQPLATQKDLTGQVPTPVVKQTKLKQRADSRESLKPAAKPLPSKSVRKESKEETP
EVTKVNHVEKPPKVESKEKVMVKKDKPVKTETKPSVTEKEVPSKEEPSPVKAEVAEKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEISSEPTPMDEMSTPRDYMSDE
TINBETESPSQEFVUITKYESSLYSQEYSKPADVTPLNGFSEGSKTDATDGKDYNASA
STISPPSSMEEDKFSRSALRDAYCSEVKASTTLDIKDSISAVSSEKVSPSKSPSLSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPSPLEKTPLGERSVNFSLTPNEIKVSAEAEVAPVSPEVTQEVVEEHCASPEDKTLEV VSSOGVYGESAGHTPYYQSPDEKSSHLTPEVTERPPAVPVSPERESABOBERSASVS PMDERVPDSESPIENSTENESPERSGKG GSPDQVSPVSSFLSADDKASGREBSPEEKSGKG GSPDQVSPVSEWISTLIYQDKQBGKSTDFAPIKEDFGQEKKTDDVEAMSQPALALDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKLGDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGVAEDTYSHMEGVASV
STASVATSSFPEPTTDDVSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTFQETEMSPSK
EECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPESEGYSYETSTKTTRTPDTSTYCYETAEKITRTPQASTYSYETSDLCYTAEKKSPS
EARQDVDLCLVSSCEYKHPKTELSPSFINPNPLEWFASEEPTEESEKPLTQSGGAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVKAARGEEKDKETKNAANASASKSAKTATACPGTTKTTKSSAVPPGLPVYLDLCYIP
NHSNSKNVDVEFFKRVRSSYYVVSGNDPAAEEPSRAVLDALLEGKAQMGSNMQVTLIP
THDSEVMREWYQETHEKQQDLNIMVLASSSTVVMQDESFPACKIEL"
RSDVLETVVLINPSDEAVSTEVRLMITDAARHKLLVLTGQCFENTGELILQSGSFSFQ
                                                                                                VNGFNMLINGGSERKSCFWKLIRHLDRVDSILLTHIGDDNLPGINSMLQRKIAELEEE
                                                                                                                                                              MKPEPLFRSVGNTIDPVILFQKMGVGKLEMYVLNPVKSSKEMQYFMQQWTGTNKDKAE
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EASPSTSSAHTPSQIASPLQEDTLSDVAPPRDMSLYASLISEKVQSLEGEKLSPKSDI
SPLTPRESSPLYSPTFSDSTSAVKEKTATCHSSSSPPIDAASAEPYGFRASVLFDTMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISEKTISPPEVSGYSYEKTERSRRLLDDISNGYDDSEDGGHTLGDPSYSYETTEKITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTKTKSSSPVKKSDGKSKPLAASPKPAGLKESSDKVSRVASPKKKESVEKAAKPTTTP
                                                                                                                                                                                                                                                                                                 ATDVKPKAAKEKTVKKETKVKPEDKKEEKEKPKKEVAKKEDKTPIKKEEKPKKEEVKK
                                                                                                                                                                                                                                                                                                                                EVKKEIKKEEKKEPKKEVKKETPPKEVKKEVKKEEKKEVKKEEKEPKKEIKKLPKDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HHLALNRDLSTPGLEKDSGGKTPGDFSYAYQKPEETTRSPDEEDYDYESYEKTTRTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGGYYYEKIERTTKSPSDSGYSYETIGKTTKTPEDGDYSYEIIEKTTRTPEEGGYSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ams region; amsA gene; amsB gene; amsC gene; amsD gene; amsE gene; amsF gene; amsK gene; amsK gene; amsK gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 1.31e+00;
0; Mismatches 12; Indels
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E, F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2212 g
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Local Similarity 73.9%;
nes 34; Conservative
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Erwinia amylovora
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JOURNAL

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FEATURES

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TITLE JOURNAL

REFERENCE

AUTHORS

DEFINITION

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KEYWORDS

ORGANISM

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RBS
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TGIPOHELDLKIATHILLSVICVGWFWVRLRHYTYRRPFWFELKEVFRILLFSIVDL
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SVSALSKWELSKWITVALTTWLLSMAWVPGRACVRRLLHRKKLWKKOSIIIGESTRAQE
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SGOSRDRWLKNLATHNCRSVSVIPSLRGVPLKGDDMAIFSHEVGNIGTGFKRCIKLR
SRPLKRTPDLVGALGIITLLLDALVILFRYSRDGGARIYGHERVGROGRKFKCLKLR
SWYVNSKBYLEEVLRTDPVARAEWDEDFKLKNDPRITRIGHFIRKTSLDELPQLWNVV
RGEMSLVGPRRVIERBLERTAGDVDYYFMARPGMTGLWQVSGRNDVSYETRYFPDSWY
VKWMSLWNDIALFRTIGVVLKRDGAY"
AGENE-"ansh"

2600...2604
//gene="ansh"
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DIDKYVNIFPPLPSLVERMKRKVVGAANATLGERLGNYEYRTGVGDLMYTWBHPE
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VDVNVASFKSGKTYVTGEVTTSGQQAIINVPLTILDAINAGGLIATADWRNVVLTHD
SROQPYSLAGALMQNDPSGNHLLYPODILYVPRNDEVKYWGEVKQQAILKMDRSGM
TLSEALGSAGGMDGYSVADATGVFVYIRPWGARRSNIANIYQLITKMDRSGM
TLSEALGSAGGMDGYSVADATGVFVIRPWGARRSNIANIYQLITKMARPEFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="minsilvycignicrsprgerllkaalperkiasaglkawyggs
ADETASIVANEHGYSLQDHYAQQLTADMCRDSDLILVMEKKHIDLYCRINPSVRGKTM
LFGHWINQQEIADPYKKSRDAFEAYYGVLENAAQKWYNALSR"
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VVADMGKDTGVLGLTYSGEDPVQISRVLDQVINNYLYQNIARKSEEAEKSIQFLAQQL
PDVRAKLDQAEDKLNVFRRKHDSVDMSLEAKSALDSSVSIQTQLNALTFREAEVSQLF
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TVADLGLDVLVQQDHFPLIGAGLSRIIGQKAQQIAVSRLKVPTLWDKRELSVEVDGPD
                                                                            Submitted (01-MAR-1994) K. Geider, MPI fuer medizinische Forschung, Jahnstr 29, 69028 Heidelberg, FRG
3 (bases 1 to 17013)
Geider, K.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="UDP-galactose-lipid carrier transferase"
/db_xref="PID:9600427"
                                                                                                                                                                                     Direct Submission
Submitted (06-DEC-1994) K.K. Geider, MPI fuer medizinische
Forschung, Jahnstr 29, 69028 Heidelberg, FRG
Location/Qualifiers
1..17013
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/db_xref="PID:g600430"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="outer membrane protein"
/db_xref="PID:9600428"
                                                                                                                                                                                                                                                                                                                    /organism="Erwinia amylovora"
507.512
530.535
1048.1051
/gene="amsG"
/gene="amsG"
/codon_start=1
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/db_xref="PID:9600429"
/transl_table=11
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/codon_start=1
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/gene="ams1"
3762..4196
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(bases 1 to 9538)
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                      Geider, K.K.
Direct Submission
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-10_signal
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HGIDNPEQLEELGLUVYASYPELSEWORKDOETLLKTOANLALDAY VS VELVLAKGLEH
SIEAIRSLRTSLHFAMMDAQNNILMTGASPGIGKTRYCANLATUPHYRLLALGNPTDL
SIEAIRSLRTSLHFAMMDAQNNILMTGASPGIGKTRYCANLATUPAKTGEKYLFIDG
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YKRRIQHGIDIKGIILNAVVRKSANNYGYGYDYYDYSYQQGEKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traislation="MKDISFSVVIPAYNASESIITTLDCLNEGSYKNFDVIIVDDKSA
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GSQHKGESVKYSLFWLDAMKPHLIRRDVYIYKAYKLPLRYKMDGKSLQASLSFARFF
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ALFESFFLLFISFTAVSTNAMYYKKYSPLILCSLCIYSAHLFINKDNNQIRFGLGSAF
ALAFICSLVARNYLLALLFIVLSTGSHSTGYTIVMIIPFFFIRERXYLPLVLVIASIP
LGGIGGKKLFELDSCGIYPVALGSRAASYSGTNEPTTSPYFGLAKLKNIRFIGAFTLYYF
RKGIMKEDRFYYILLIAYSIGAAVRITFSDFSİFGGRYĞNLFHTEPLLFAFLMIRRIR
NILLNFFMLFSITTYYLAYNTILSAPSIMGYSVAPLFRIFS"
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DKVISAGSYQHHLYMEDYNDALRIMSLGHPYANLPDVLMKVRAGSDMYNKRRGWNYIK
SEVQLYRLKLALKQTGFIRGTLYFLIRTMTRLMPVKVMQFLYEKDRKG"
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VRRLLCOEDHYSIETLSAAVRKLKVFCYGLAEKVVLYDHDWRVYLTAFSEKNVYVYO
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DGEEKAELLEKIKKYHLEESAEIVSPSKKISEYYRSSGVIAMTSRYEGLEWYLIERAN
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lsopidlnsetlktfyaakgalwsaseysmalhndndeoifyypdyknngysefsrrl
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QQELNISKASTVGDVRIIDHAETAAKPVAPKSILIVAGSLILGLVVSVGLVLMKALFH
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                                                                                                                                                                                                                                                                                                                                                                                                          /product="glycosyl transerase"
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/db_xref-"PID:g600433"
/+rancl +-1.
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9775..10575
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8707..9762
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7414..8541
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/gene="amsD"
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/gene="amsF"
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/gene="amsF"
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Gaps

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/codon_start=1
/product="8 kDa outer arm dynein light chain"
/product="8 kDa outer arm dynein light chain"
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ELHVRNPFGOVPALODGDLYLFESRAICKYARKNREELLREGNLEERAMVDWNIEVE
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LSLADLNHVSYTLCLFATFYASVLDAYPHYRAWWSGLMERPSVOKYAALMKPGA"
                                                                     'clone_lib="lambda ZAPII cDNA made from cells regenerating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (Dases 1 to 1671)
Shah, D.M., Hironaka, C.M., Wiegand, R.C., Harding, E.I., Krivi, G.G.
and Tiemeler, D.C.
Structural analysis of a maize gene coding for glutathione-S-
transferase involved in herbicide detoxification
Plant Mol. Biol. 6, 203-2211 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tacatcaagaaggagttcgaccggaagcacaacccgacgtggcactgcatcgtcggccgc 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MZEGSTIA2 1671 bp DNA PLN 15-SEP-1989
Maize glutathione S-transferase gene (GST-I), exons 2 and 3.
M16902
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                                                                                                                                                                                                                                                                                                                                                                                    Length 683;
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join(M16900:246..395,238..286,956..1401)
/note="glutathione S-transferase I"
                       /organism="Chlamydomonas reinhardtii"
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                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 61; 1
Pred. No. 5.68e+00;
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                                               /strain="1132D"
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glutathione transferase.
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Best Local Similarity 66.7%;
Matches 42; Conservative
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                                                                                                     flagella"
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                                                               ISFEQIERSPNGGGFFHNICPAGOYFRGSCLRFTGGGGVSLSLIDTLDCKIDOWYAS
KCTGDVIRGSWSFTKKGNWDHNTAIELSNFNVOHCROGKVLNLPRCTGSIIHNGWIEH
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RRFSLHNGLAGIGANEGODLLVESRHIDAAKVETSRAEGYISLVINGQOVAVPYFALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFTDKLKQYDAVIQVGGSFFVDLYGPLQFEHSLCALLAKKPVYMIGHSVGPFQKERFN
QOARPYESRVNSLVLRESVSLEMMERAGITTQKVIPQADTAFLYRTRTLDAFGHNLIH
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MNFGTPAVAINYEHKSLGYWKQLGLPEMASDVQSLMDGSIIAKVKGVLDNYEEMEQQV
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SKLLLPAIVAANKKPFAADIFLVHFGYAGALANKLRELKVLQGKQVTVFHGADISRRH
ILEEHKKDYPRLFAQNELLLPISRLWGHKLIAMGCPAEKINVTRMGIEPEKFNLKLRD
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                     Y IASSGQDFHWRRVSDDMNRITLFDFGAVADGKKDCLPAVMAMYHWAQNNNQKLSIQF
PAGRFFISSFDISAKYIRFLRLAGAPVNFGYFPATTLASDGKSEFLFKVNARWVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKILLVGNHTCGNRGDGAILRGIIDSLHLERTDLDIDIISRFPT
SSSYLLQQNIWPDELFLETKKSNSLVAKVKRRLMPKIMMAHIRGSGFFKNLAVPEYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKLTFFTMQFPVSSETFVLNQVTHFIDIGYDVEIIAVFPGDLVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRU19490 683 bp mRNA PLN 08-NOV-1995
Chlamydomonas reinhardtii 8 kDa outer arm dynein light chain mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryoteae; mitochondrial eukaryotes; Viridiplantae; Chlorophyta;
Eukaryoteae; witochondrial eukaryotes; Viridiplantae; Chlorophyta;
Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

(bases 1 to 683)
King, S.M. and Patel-King, R.S.
The M(r) = 8,000 and 11,000 outer arm dynein light chains from Chlamydomonas flagella have cytoplasmic homologues
Chlamydomonas flagella have cytoplasmic homologues
95.263466
2 (bases 1 to 683)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgctgttcagcgcgatcatgtatctggccatcggcatt 16425
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14283..14286
/gene="amsk"
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/db_xref="PID:9600436"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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13042 ..14289
/gene="amsJ"
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/gene="amsK"
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/organism="Sus scrofa"
93..1865
/note="muscarinic acetylcholine receptor III (AA 1 - 590)"
                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus. 1 (bases 1 to 1913)
Akiba,I., Kubo,T., Maeda,A., Bujo,H., Nakai,J., Mishina,M. and Numa,S.
Primary structure of porcine muscarinic acetylcholine receptor III and antagonist binding studies
FEBS Lett. 235 (1-2), 257-261 (1988)
                ô
                                                                                                                         SSACHRM 1913 bp DNA MAM 12-SEP-1993 Porcine DNA for muscarinic acetylcholine receptor III. x12712
                Gaps
              0
Best Local Similarity 78.4%; Pred. No. 5.68e+00;
Matches 29; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                     library=lambda EMBL3; clone=pSpmACR7.
Data kindly reviewed (03-OCT-1989) by Numa S.
Location/Qualifiers
                                       acetylcholine receptor.
                                                                                                                                                                                                                                                                                                                                                                                             1..1913
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Sus scrofa
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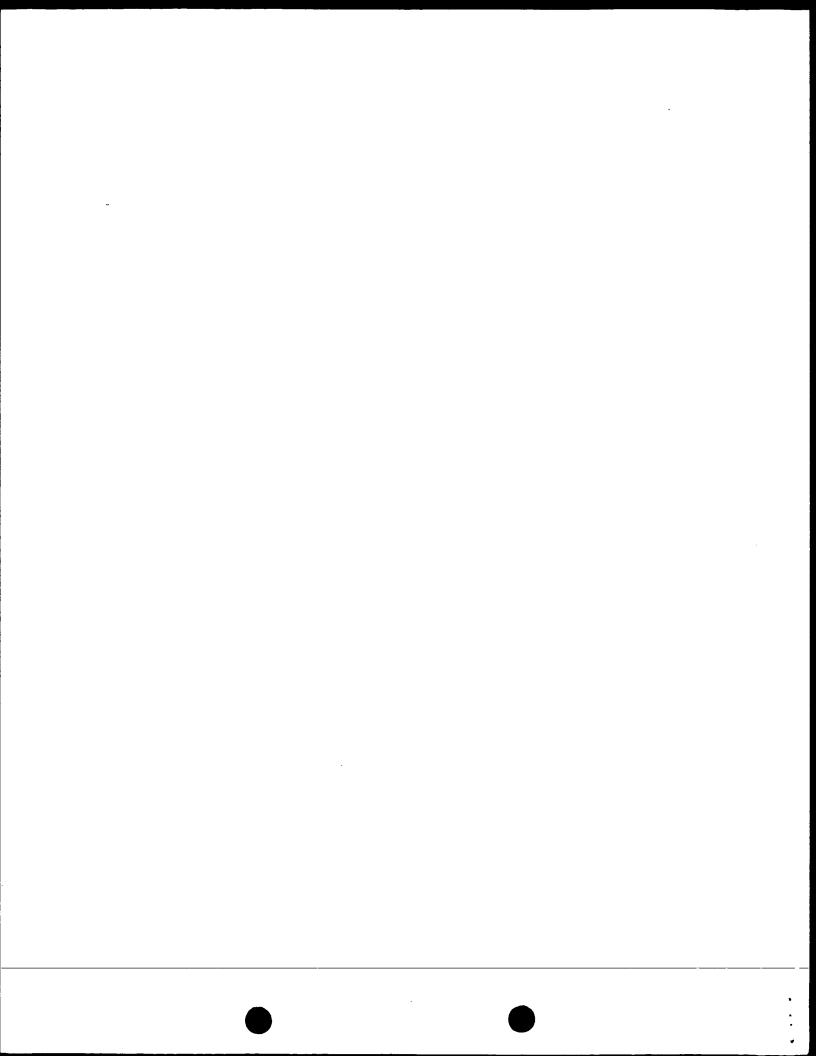
Gaps ô Match 4.8%; Score 21; DB 48; Length 1913; Local Similarity 83.9%; Pred. No. 5.68e+00; es 26; Conservative 0; Mismatches 5; Indels Query Match lest Local Si Matches 26

ORIGIN

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Search completed: Tue Dec 2 17:21:44 1997 Job time : 415 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn Tue Dec 2 17:22:01 1997; MasPar time 56.86 Seconds 803.956 Million cell updates/sec Run on:

not generated alar output

>US-08-915-004-14 (1-438) from US08915004.seq 438 Description: Perfect Score: tle:

......AGCCACAGATATGTATCTGA 438 1 ATGAACAAGTTGCTGTGCTG. TACTTGTTCAACGACACGAC Sequence:

N.A.

TABLE default Gap 6 Scoring table:

Query 0 Dbase 0; STD Nmatch 142080 seqs, 52183452 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseg28 Database:

Mean 8.240; Variance 4.524; scale 1.822

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	Ð	Description	Pred. No.
-	438	100.0	438	28	T36689	Osteoclastoqenesis in	0.00e+00
7	402	91.8	1173	28	T35475	Human tumour necrosis	4.15e-284
m	400	91.3	432	27	T33176	Mutated OCIF, OCIF-CC	1.48e-282
4	400	91.3	564	27	T33180	Mutated OCIF, OCIF-CB	1.48e-282
Ŋ	400	91.3	594	27	T33175	Mutated OCIF, OCIF-CD	1.48e-282
9	400	91.3	819	27	T33174	Mutated OCIF, OCIF-CD	1.48e-282
7	400	91.3	996	27	T33179	_	1.48e-282
ω	400	91.3	981	27	T33170	Mutated OCIF, OCIF-DD	1.48e-282
σ	400	91.3	984	27	T33171	Mutated OCIF, OCIF-DD	1.48e-282
10	400	91.3		27	T33173	Mutated OCIF, OCIF-CC	1.48e-282
11	400	91.3		27	T33169	Mutated OCIF, OCIF-DC	1.48e-282
12	400	91.3	1182	27	T33178	Mutated OCIF, OCIF-CB	1.48e-282
13	400	91.3		27	T33172	Mutated OCIF, OCIF-CL	1.48e-282
14	400	91.3		27	T33164	Mutated OCIF, OCIF-C2	1.48e-282
15	400	91.3	1206	28	T36685	Osteoclastogenesis in	1.48e-282

Ouery Match 100.0%; Score 438; DB 28; Length 438; Best Local Similarity 100.0%; Pred. No. 0.00e+00;

883 2027 2027 2027 2020 2020 2020 2020 202	
Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C1 Mutated OCIF, OCIF-C2 Mutated OCIF, OCIF-C5 Mutated OCIF, OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF, OCIF-C6 Mutated OCIF-C6 Mutated OCIF, OCIF-C7 Mutated OCIF, OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated OCIF-C6 Mutated	O O O O O O O O O O O O O O O O O O O
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1116 1116 1118 1118 1118 1118 1118 1118	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
υ υυ	0 0 0 0

ALIGNMENTS

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ONA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis Claim 24; Page 76; 183pp; Japanese.
This sequence encodes full length osteoclastogenesis inhibitory factor (OCIF) 5. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducting conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g.
                     22-ARR-1997 (first entry)
Osteoclastogenesis inhibitory factor 5 coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ss.
                                                                                                                                                                                                                                                                                Morinaga
Yasuda H;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
NAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
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                                                                                                         Location/Qualifiers 1..63
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 BP
 standard; DNA; 438
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W09626217-A1
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mat_peptide
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To treating e.g. tumours, infection, auto:immune disease, graft rejection, cytotoxicity or inflammation

Claim 1; Fig 1; 59pp; English.

Claim 1; Fig 1; 59pp; English.

Claim 1; Fig 1; 59pp; English.

Claim 1; Fig 1; 59pp; English.

Claim 1; Fig 1; 59pp; English.

Claim 1; Fig 1; 59pp; English.

Claim 1; Fig 1; 59pp; English.

Claim 1; Fig 1; 59pp; English.

The receptor binds to TNF, and in particular, TNF-beta.

The receptor may be used for screening for antagonists and agonists of the receptor and for liquads for the receptor. Such agonists may differentiation, to mediate the immune response and anti-viral response, to requiate growth and provide resistance to certain infections. The antagonists may be used therapeutically, to treat untofinned diseases, inflammation, septic shock, to inhibit graft-versus-host reactions, and to prevent apoptosis.

Sequence 1173 BP; 374 A; 277 C; 265 G; 257 T;
                                                                                                                                                                                                                                                                                           360
                                                                             caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                                                                                           tgtgacaaatgteeteetggtacetacetaaaacaacactgtacagcaaagtggaagace 180
                                                                                                                                                                                   gigigococcitgococtgaccactactacacagacagctggcacaccagtgacgagtgt 240
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                                      atgaacaagttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1997 (first entry)
Human | tumour necrosis factor receptor.
Tumour necrosis factor, TNF, receptor; TNF-beta; ligand; tumour;
differentiation; immune response; autoimmune disease; inflammation;
septic shock; graft-versus-host; apoptosis; ss.
                                                                                                                                              | deatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
                                                                                                                                                                                                           GIGIGCGCCCTTGCCCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGT
                                                                                                                                                                                                                                                                                          ¢acaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa
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0; Mismatches
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15-WAR-1995; U03216.
15-WAR-1995; WO-U03216.
29-MAR-1995; ZA-002587.
(HUWA|) HUMAN GENOME SCI INC.
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WPI; 96-433821/43.
P-PSDB; R99357.
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/*tag= a
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ID T3
AC T3
AC T3
DT 05
DE HU
KW d1
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To be provided the control, esp. treatment of osteoporosis or claim 72; Agaper : 183pp; Japanese.

To bone resorption control, esp. treatment of osteoporosis or claim 72; Agaper : 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CCR4 in which amino acids 123-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the protein sequence and the wild type OCIF CNRA sequence given in 736685.

Sequence 432 BP; 116 A; 117 C; 106 G; 93 T;
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Mutated OCIF, OCIF-CCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
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                                                                                                                                                                                                                      1 atgaacaagttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                                                                                                                                                                                            1 AIGAACAAGTIGCIGIGCIGCGCCCCCGIGITICIGGACAICICCATIAAGIGGACCACC 60
                                                                                                                      Gaps
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29-AUG-1996.

70-AUG-1996.

PR 20-FEB-1995; JP-054977.

PR 21-JUL-1995; JP-207508.

PR 31-JUL-1995; JP-207508.

PR 31-JUL-1995; JP-207508.

PR 41-JUL-1995; JP-207508.

PR 41-JUL-1995; JP-207508.

PR 21-JUL-1995; JP-
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0
     Score 402; DB 28; Length 1173;
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                                                              Pred. No. 4.15e-284;
                                                                                                                0; Mismatches
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T33176 standard; DNA; 432 BP.
ch 91.8%;
1 Similarity 100.0%;
402; Conservative
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/product= OCIF-CCR4
WO9626217-A1.
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Synthetic.
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mat_peptide
Query Match
                                                                   Best Local
                                                                                                           Matches
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124 T;

132 G;

149 C;

159 A;

564 BP;

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for bone resorption control, esp. treatment factor process.

Claim 84; Page 149-150; 183pp; Japanese.

Claim 84; Page 149-150; 183pp; Japanese.

This sequence encodes a mutated version of the full length
osteoclastogenesis inhibitory factor (OCIF) of the invention. This
sequence encodes OCIF-CBSp in which amino acids 167-380 of the mature
protein have been deleted. These amino acid changes have been caused
by the introduction of a restriction site. The OCIF of the invention
has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
and 120 kD under non-reducing conditions. The protein is adsorbed onto
cation-exchangers or heparin and its activity is lowered after 10 mins
at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 50
deg.C. OCIF is useful in the control of bone resorption and therefore
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                           121 tytgacaaatgtoottootggtacotaacotaaaacaacactgtacagoaaagtggaagaco 180
                                                                                                                                                                                                                                              241 CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC 300
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                                     Gaps
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                                                                        1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc
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Yasuda H;
Length 432;
                                     Indels
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20-FEB-1995; JP-054897.
21-012-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                         ..
Score 400; DB 27; Pred. No. 1.48e-282;
                                   0; Mismatches
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T33180 standard; DNA; 564 BP
Query Match
Best Local Similarity 99.8%;
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                                     401; Conservative
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for bone resorption control, esp. treatment of osteoporosis claim 69; Page -; 183pp; Japanese.

Claim 69; Page -; 183pp; Japanese.

Claim 69; Page -; 183pp; Japanese.

Claim 69; Page -; 183pp; Japanese.

Sequence encodes a mutated version of the full length

osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CDD1 in which amino acids 177-380 of the mature protein have been deleted. The OCIF of the invention and 120 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis. This sequence is not given in the specification and is derived from the
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                                                                                                                                                                                              61 CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCAGTT 6 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1997 (first entry)
Mutated OCIF, OCIF-CDD1, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                     1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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                              91.3%; Score 400; DB 27; Length 564;
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                                                                   Indels
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20-FEB-1996; JO0374.
20-FEB-1995; JP-05497.
21-ULE-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, P-PSDB; R99945.
                                                Pred. No. 1.48e-282;
                                                                   0; Mismatches
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T33175 standard; DNA; 594 BP.
T33175;
                                                  99.88;
                                                                   401; Conservative
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                                                  Best Local Similarity
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Synthetic.
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mat_peptide
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim [6:, Page 145: 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CDD2 in which amino acids 252-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 70 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
                                                                                                 ö
protein sequence and the wild type OCIF cDNA sequence given in T36685. Sequence 594 BP; 176 A; 152 C; 136 G; 130 T;
                                                                                                                                                                                                                                                                                         tgtgacaaatgtcctcctggtacctacctaaaacaacatgtacagcaaagtggaagacc 180
                                                                                                                                                                                                                                                                                                               121 jGTGACAAATGTCCTCCTGGTACCTACTAAAACAACACTGTACAGCAAAGTGGAAGACC 180
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301 qacaaccgggtgtgcgaatgcaaggagggggtaccttgagatagagtgtgggttgaaa 360
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                   1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Yasuda H;
                                                             Length 594;
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW |) SNOW BRAND MILK PROD CO LTD.
Goto M, Higashlo K, Kobayashi F, Mochizuki S,
Nakaqawa N, Shima N, Tsuda E, Ueda M, Yano K,
P-PSDB; R99944.
                                                       Score 400; DB 27; I
Pred. No. 1.48e-282;
                                                                                               0; Mismatches
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                                                     Query Match
Best Local Similarity 99.8%;
Matches 401; Conservative
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WO9626217-A1.
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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis

Claim 81; Page 149; 183pp; Japanese.

Claim 81; Page 149; 183pp; Japanese.

Claim 81; Page 149; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CSph in which maino acids 298-380 of the mature osteoclastogenesis inhibitory factor (OCIF) of the invention of a restriction site. The OCIF of the invention has a molecular weighth by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg. C. OCIF is useful in the control of bone resorption and therefore in the treatment and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
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Mutated OCIF, OCIF-CSph, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
WPI; 96-402320/40.
                                                           / Match 91.3%; Score 400; DB 27; Length 819; Local Similarity 99.8%; Pred. No. 1.48e-282; nes 401; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 cataggagctgccctcctggatttggagtggtgcaagctgga 402
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188 G;
198 C;
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20-FEB-1995; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
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251 A;
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W09626217-A1.
819 BP;
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Sequence
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218 G;

238 C;

312 A;

981 BP;

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DNA encoding osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 51, Page 141-142; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-DDD1 in which amino acids 178-252 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                                                                 121 TGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGGAAAGTGGAAGACC 180
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22-APR-1997 (first entry)
Wutated OCIF, OCIF-DDD1, coding sequence.
Osteoclastogenesis inhibitory factor: OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                           61 CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG 120
                                                                                                                                                      1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC 60
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prevention of disorders of bone resorption, e.g. osteoporosis. Sequence 966 BP; 301 A; 228 C; 226 G; 211 T;
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                                                          Length 966;
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI; 96-402320/40.
                                                                            Pred. No. 1.48e-282;
                                                          DB 27;
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T33170 standard; DNA; 981 BP.
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99.88;
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Synthetic.
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Division of the control, esp. treatment of osteoporosis claim of the mendaling osteoclastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 57; Page 142-143; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes off-DDD2 in which amino acids 253-326 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under on reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-DDD2, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                              61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                                                                                                                                                                                                                 61 CAGGAAACGITICCICCAAAGIACCIICATIAIGACGAAGAAACCICICAICAGCIGIIG 120
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                                                                                                          1 atgaacaacttgctgttgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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                              DB 27; Length 981;
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W09656217-A1.
W09656217-A1.
20-FB2-1996; JD0374.
20-FB2-1995; JP-054977.
21-JUL-1995; JP-054977.
(SNOW) SNOW BRAND MILK PROD CO LTD.
GOLO M, H1gashlo K, Kobayashi F, Mochizuki S, Mo
WPI; 96-402320/40.
P-PSDB; R99941.
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                              Score 400; DB 27; I
Pred. No. 1.48e-282;
0; Mismatches 1;
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Best Local Similarity 99.8%;
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                                                                                                          tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
                                                                                                                                             gtgtgcgccccttgccctgaccactactacacagacagctggcacaccagtgacgagtgt 240
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Mutated OCIF, OCIF-CC, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
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                                    atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                     1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTTTTCTGGACATCTCCATTAAGTGGACCACC 60
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 Length 984;
                   1; Indels
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 Score 400; DB 27; I
Pred. No. 1.48e-282;
0; Mismatches 1;
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 91.3%;
                 401; Conservative
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Best Local Similarity
Matches 401; Conserv
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22-APR-1997 (first entry)
Mutated OCIF, OCIF-DCR4, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                      1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                                                                                           9
                                                            Gaps
                                                                                                                                                      1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTTTTCTGGACATCTCCATTAAGTGGACCACC
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          Length 1056;
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Yasuda H;
                                                          Indels
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29-AUG-1996.
20-FEB-1996.
20-FEB-1995.
21-JUL-1995; JP-207508.
21-JUL-1995; JP-207508.
GSNOW BRAND MILK PROD CO LTD.
GOCO M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, WPI: 96-402320/40.
     Score 400; DB 27; L
Pred. No. 1.48e-282;
0; Mismatches 1;
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       91.3%;
Query Match 91.3%;
Best Local Similarity 99.8%;
Matches 401; Conservative
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Synthetic.
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91.3%; Score 400; DB 27; Length 1080;

Query Match

US-08-915-004-14.rng

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Query Match

91.3%;

Best Local Similarity 99.8%;

Matches 401; Conservative
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Claim 78; Age 148; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CBst in which Gln371 is substituted with Leu and amino acid changes have been caused by the introduction of a restriction site. The OCIF of the invention has a molecular weight by SDS-PAGE of the whole treducing conditions and 120 Kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Mutated OCIF, OCIF-CBst, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                      61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                                                                                                                         61 CAGGAAACGTTTCCTCCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG 120
                                                                                                                                                                                                                                                       GIGIGGGCCCCTIGCCCTGACCACTACTACACAGACAGCTGGCACACCAGTGACGAGTGT 240
                                                                                                                                                                                                                                                                                                                                              cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa 360
                                                                          1 ATGAACAAGTTGCTGTGCTGCGCTCGTGTTTCTGGACATCTCCATTAAGTGGACCACC 60
                                              1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                  Gaps
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Yasuda H;
                  Indels
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20-FEB-1996; J00374.
20-FEB-1996; JP-054977.
21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
Hidashio K, Kobayashi F, Mochizuki S,
    Pred. No. 1.48e-282;
                  Mismatches
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Nakagawa N, Shima N, Tsuda E, Ueda M,
WPI; 96-402320/40.
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T33178;
    Best Local Similarity 99.8%;
                    401; Conservative
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mat_peptide
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Dry Book of Steedlastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis claim 60; Page 143-144; 183pp; Japanese.

This sequence encodes a mutated version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-CL in which amino acids 379-380 of the mature protein have been deleted. The OCIF of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore in the treatment and prevention of disorders of bone resorption, e.g. osteoporosis.
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Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                      tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
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                                                                                                            1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                       0; Gaps
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Length 1182;
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                                                          Indels
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21-JUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
NAKAGAWA N, Shima N, Tsuda E, Ueda M, Yano K,
WPI; 96-402320/40.
                                                       1;
  Score 400; DB 27; I Pred. No. 1.48e-282;
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                                                       0; Mismatches
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T33172 standard; DNA; 1200 BP.
T33172;
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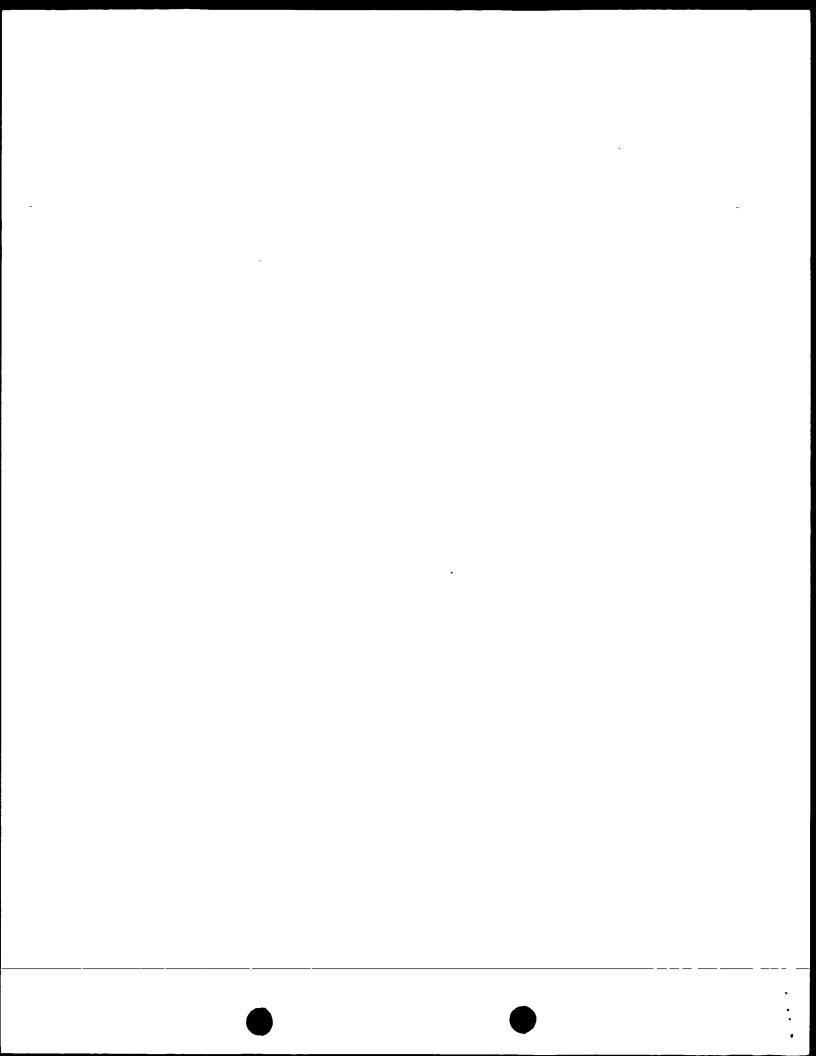
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This sequence encodes a mutaded version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes a mutade version of the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. This sequence encodes OCIF-C22S in which the 22nd Cys residue in the mature OCIF protein is substituted by Ser. The OCIF of the invention has a molecular weight by SDS-PREF of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation—exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. or 30 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and therefore on the control of the control of bone resorption of e.g.
                                                                                                                               caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
                                                                                                                                                    61 ¢AGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG 120
                                                                                                                                                                                                                            tgtgacaaatgtcctcctggtacctacctaaaaacaacactgtacagcaaagtggaagacc 180
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                                                                                                                                                                                                                                                                                                                  181 GTGTGCGCCCTTGCCCTGACCACTACTACAGAGGGGGCTGGCACACCAGTGACGAGTGT 240
                                                                                                                                                                                                                                                                                                                                                         ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300
                                                                                                                                                                                                                                                                                                                                                                                                                                301 cacaaccgcgtgtgcgaatgcaaggaagggcgctaccttgagatagagttctgcttgaaa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1997 (first entry)
Mutated OCIF, OCIF-2225, coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                           241 cTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACC 300
                                                        atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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                       1; Indels
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20-FEB-1996; JO0374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW |) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashio K, Kobayashi F, Mochizuki S,
Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K,
P-PSDB; R99934.
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Best Local Similarity 99.8%; Pred. No. 1.48e-282;
                       0; Mismatches
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T33164 standard; DNA; 1206 BP.
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                     401; Conservative
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W09626217-A1.
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                   Matches
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                                                                                                                                                                                         tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osteoclastogenesis inhibitory factor coding sequence.
Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
                                                  1 atgaacaacttgctgttgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
                                                                                 1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTTTTCTGGACATCTCCATTAAGTGGACCACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For the process of the protein of the protein of the protein of the conding osteoclastogenesis inhibitory factor protein of the bone resorption control, esp. treatment of osteoporosis. This sequence encodes the full length osteoclastogenesis inhibitory factor (OCIF) of the invention. The OCIF has a molecular weight by SDS-PAGE of 60 kb under reducing conditions and 120 kb under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C or 10 mins at 56 deg.C. and is lost after 10 mins at 90 deg.C. OCIF is useful in the control of bone resorption and the resorption, e.g.
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          121 IGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACC
                                                                                                                                                                                                                                                                                                                                241 ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc
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                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 cataggagctgccctcctggatttggagtggtgcaagctgga 402
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Best Local Similarity 99.8%; Pred. No. 1.48e-282; Matches 401; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goto M, Higashio K, Kobayashi F, Mochizuki S, Nakagawa N, Shina N, Tsuda E, Ueda M, Yano K, WPI: 96-402320/40.
P-PSDB; R99924-25.
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20-FEB-1996; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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T36685 standard; DNA; 1206 BP
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w09626217-A1.
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Search completed: Tue Dec 2 17:23:02 1997 Job time: 61 secs.



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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Tue Dec 2 17:23:26 1997; MasPar time 278.32 Seconds 807.828 Million cell updates/sec Run on:

lar output not generated.

>US-08-915-004-14 (1-438) from US08915004.seq 438 itle: Description: Perfect Score: N.A. Sequence:

......AGCCACAGATATGTATCTGA 438 1 ATGAACAAGTTGCTGTGCTG. TACTTGTTCAACGACACGAC.

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD : Nmatch

707517 seqs, 256659390 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Database:

EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

9:EST9 10:EST10 11:EST11 18:EST12 13:EST13 14:EST14

15:EST9 15:EST16 11:EST11 18:EST13 14:EST14

15:EST9 20:EST20 20:EST20 20:EST20 20:EST30

21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26

23:EST33 34:EST34 35:EST35 30:EST30 31:EST31 32:EST30

39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44

45:EST45 46:EST46 47:EST47 48:EST42 43:EST43 44:EST40

51:EST51 58:EST5 53:EST53 54:EST40 43:EST40 65:EST56

57:EST57 56:EST52 53:EST53 54:EST40 43:EST40 65:EST56

69:EST69 70:EST70 71:EST71 72:EST70 73:EST70 74:EST70

75:EST75 76:EST76 77:EST77 72:EST77 73:EST70 74:EST70

81:EST81 82:EST8 89:EST88 89:EST89 90:EST90 91:EST91 92:EST90

93:EST99 46:EST94 95:EST95 96:EST96 97:EST97 98:EST90

94:EST99 47:EST90 77:EST10 102:EST102 103:EST103 104:EST1104

100:EST100 111:EST101 102:EST107 108:EST103 104:EST1104

110:EST110 111:EST111 112:EST112 113:EST113 114:EST112

120:EST120 121:EST121 122:EST122 123:EST133 134:EST124

135:EST135 136:EST136 137:EST137 138:EST133 134:EST124

135:EST135 136:EST136 137:EST137 138:EST138 139:EST139

140:EST110 111:EST111 112:EST112 113:EST113 134:EST114

115:EST113 136:EST114 142:EST117 118:EST113 134:EST114

115:EST113 136:EST114 142:EST112 123:EST123 134:EST124

136:EST136 136:EST136 137:EST137 138:EST138 139:EST139

137:EST135 136:EST136 137:EST137 138:EST138 139:EST139

140:EST110 111:EST111 112:EST112 113:EST113 134:EST114

145:EST1136 136:EST136 137:EST137 138:EST138 139:EST139

140:EST131 144:EST144 147:EST117 148:EST144

145:EST135 136:EST136 137:EST137 138:EST138 139:EST139

140:EST137 146:EST146 147:EST137 138:EST138 139:EST139

150:EST136 136:EST136 137:EST137 138:EST138 139:EST139

165:EST136 166:EST146 147:EST137 138:EST138 139:EST139

165:EST136 166:EST136 167:EST137 138:EST138 139:EST139

165:EST136 166:EST166 167:EST167 168:EST168 169:EST

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175:EST175 176:EST176 177:EST177 178:EST178 179:EST179 180:EST180 181:EST181 182:EST182 183:EST183 184:EST184 185:EST186 186:EST186 187:EST187 188:EST188 189:EST189 190:EST190 191:EST191 192:EST192 193:EST194 195:EST196 197:EST197 198:EST198
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Mean 10.031; Variance 1.782; scale 5.629 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. N	sapie 2.49e-07	tagene 6.10e-	sthal 6.10e-06	tial se 6.10e-0	ares pre 6.10e-	stina cD 6.10e-0	clone 1.34e-0	sapie 1.34e-0	reatic 1.34e-	ne-free 1.34e-	Toxop 1.34e-0	sapie 1.34e-0		0.010	sapie 1.34e-0	sapie 1.34e-04 sapie 1.34e-04	sapie 1.34e-04 sapie 1.34e-04 res ret 1.34e-0	sapie 1.34e-04 sapie 1.34e-04 res ret 1.34e-0 res ret 1.34e-0	sapie 1.34e-0 sapie 1.34e-0 es ret 1.34e- es ret 1.34e- itagene 1.34e-	saple 1.34e-04 saple 1.34e-04 res ret 1.34e-0 tres ret 1.34e-0 res pre 1.34e-0 saple 2.59e-03	saple 134e-04 saple 134e-04 es ret 134e-0 res ret 134e-0 res ret 134e-0 res ret 134e-0 res pre 134e-0 saple 259e-03	saple 1.34e-04 cs rat 1.34e-04 cs ret 1.34e-0 ttagene 1.34e-0 saple 2.59e-03 saple 2.59e-03	saple 1.34e-04 es rapie 1.34e-04 res ret 1.34e-0 tragene 1.34e-0 tragene 1.34e-0 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03	sapie 1.34e-04 sapie 1.34e-04 res ret 1.34e-0 itagene 1.34e-0 itagene 1.34e-0 sapie 2.59e-03 sapie 2.59e-03 sapie 2.59e-03 sapie 2.59e-03 sapie 2.59e-03	saple 134e-04 es aple 134e-04 es ret 134e-0 es ret 134e-0 es ret 134e-0 es per 134e-0 es per 159e-03 saple 259e-03 saple 259e-03 saple 259e-03 saple 259e-03	saple 134e-04 saple 134e-04 cs ret 134e-0 cs ret 134e-0 cs ret 134e-0 cs pre 134e-0 cs	saple 134e-04 cs rapie 134e-04 cs ret 1.34e-0 cs ret 1.34e-0 cs pre 1.34e-0 cs pr	saple 1.34e-04 saple 1.34e-04 ces ret 1.34e-04 tragene 1.34e-0 ces pre 1.34e-0	saple 134e-04 saple 134e-04 cs ret 1.34e-0 cs ret 1.34e-0 cs ret 1.34e-0 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 region 2.59e-03 caple 2.59e-03	saple 1 34e-04 es aple 1 34e-04 es ret 1 34e-04 es ret 1 34e-0 es ret 1 34e-0 es pre 1 34e-0 es pre 1 59e-03 saple 2 59e-03 saple 2 59e-03 saple 2 59e-03 saple 2 59e-03 saple 2 59e-03 saple 2 59e-03 es pre	saple 134e-04 es rapie 134e-04 es ret 1.34e-0 tragene 1.34e-0 es pre 1.34e-0 es pre 1.34e-0 es pre 1.34e-0 es pre 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 es pre 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0 es fet 2.59e-0	saple 134e-04 cs rat 134e-04 cs rat 134e-04 cs rat 134e-0 cs rat 134e-0 cs pre 134e-0 cs pre 134e-0 cs pre 134e-0 cs pre 134e-0 cs pre 134e-0 cs pre 134e-0 cs pre 134e-0 cs pre 134e-0 cs pre 134e-0 cs fet 2.59e-0	saple 1.34e-04 es raple 1.34e-04 es rat 1.34e-0 es rat 1.34e-0 es rat 1.34e-0 es pp 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 es fat 2.59e-03	saple 134e-04 es saple 134e-04 es ret 134e-04 es ret 134e-0 es ret 134e-0 es pre 134e-0 es pre 134e-0 es pre 134e-0 es pre 134e-0 es pre 259e-0 es pre 259e-0 es pre 259e-0 es fet 259e-0	saple 134e-04 cs rat 1.34e-04 cs rat 1.34e-04 cs rat 1.34e-0 cs pre 1.34e-0 cs pre 1.34e-0 cs pre 1.34e-0 cs pre 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 cs fet 2.59e-0	saple 1.34e-04 es raple 1.34e-04 es ret 1.34e-04 es ret 1.34e-0 es per 1.34e-0 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03	saple 134e-04 saple 134e-04 ces ret 1.34e-0 ces pre 1.34e-0 ces pre 1.34e-0 ces pre 1.34e-0 ces pre 1.34e-0 ces pre 2.59e-0 saple 2.59e-0 saple 2.59e-0 saple 2.59e-0 saple 2.59e-0 ces fet 2.59e-0	saple 134e-04 es apple 134e-04 es ret 1.34e-04 es ret 1.34e-0 es ret 1.34e-0 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 es pet 2.59e-03	saple 134e-04 es saple 134e-04 es ret 134e-04 es ret 134e-0 es ret 134e-0 es pre 134e-0 es pre 134e-0 es pre 134e-0 es pre 259e-03 saple 259e-03 saple 259e-03 es pre 259e-03	saple 134e-04 saple 134e-04 ies ret 1.34e-04 ies pet 1.34e-0 ies pet 1.34e-0 ies pet 1.34e-0 ies pet 1.34e-0 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03 saple 2.59e-03
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ALIGNMENTS

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SOURCE

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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopteray11; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Butheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 258.
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    Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. Wash U-Merck EST Project
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                                                                                                       Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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300 bp mRNA EST 28-OCT-1996 550527 5'. Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone AA100384
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia: Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archorta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 344)
11 lier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Materston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
High quality sequence stops: 313
Source: IMAGE Consortium, LLNL, LALL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tel: 314 286 1800
Fax: 314 286 1810
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WashU-Merck EST Project
Washington University School of Medicine
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Pred. No. 2.49e-07;
0; Mismatches 8.
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                                                                                                                                                                                                                                                                                                                                                            midbrain, pons and medulla.
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116 c
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Best Local Similarity 77.8%;
Matches 28; Conservative
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EST(expressed sequence tag). Oryza sativa (8 days old) cDNA to
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                                                                                                                                                                                                                                                   27-JUL-1995
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Bukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 687)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Hollman, M., Hultman, M., Kucaba, T., Ech., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 cgggtgcantnacggcaaccaggtgctcaaggagctngaggaggccaagaaggngt 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 CGAGTGTCTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGT 289
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Lilopsida; Poales; Poaceae; Oryza.
1 (bases 1 to 493)
Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from shoot
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                                                                                                                 365 gaaacagttgctgnaagctaccttgagtttgcccaagaaacccttnatnag 415
                                                                                                                                                         64 GAAACGITICCICCAAAGIACCITCATIAIGACGAAGAAACCICICAICAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 493;
                         Length 472;
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/dev_stage="Green shoot (8 days old)"
/ 147 c 150 g 93 t 5 others
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Pred. No. 6.10e-06;
0; Mismatches 19; Indels
                                                                    0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute of Agrobiological Resources 2-1-2 Kanondai
                       Score 22; DB 57; I
Pred. No. 6.10e-06;
                                                                                                                                                                                                                         RICS15559A 493 bp mRNA
Rice CDNA, partial sequence (S15559_1A).
048963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-Feb-1995) to DDBJ
Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                     Ouery Match 5.0%;
Best Local Similarity 68.6%;
Matches 35; Conservative
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Best Local Similarity 66.1%;
Matches 37; Conservative
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Phone: 0298-38-7441
Fax : 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsukuba Ibaraki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frabidopsis thaliana
Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;
Brassloaceae; Arabidopsis.
1 (bases 1 to 472)
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1 (bases adores a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                          Email: estewatson.wustl.edu
High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1995
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MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 111; Length 453;
Pred. No. 6.10e-06;
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142477
19933235
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/clone="113K15T7"
/strain="var columbia"
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                                                                  WashU-Merck EST Project
Washington University School of Medicine
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MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"/clone="264865"
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu.
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Best Local Similarity 77.5%;
Matches 31; Conservative
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66
                                               Contact: Wilson RK
Unpublished (1995)
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LOCUS

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Gaps

Gaps

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/note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI; Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library. Inserts from retina cDNA library andonly primed, PCR amplified, size-selected, and cloned into lambda gt10. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR
                                                                                                                                                                             products were used for sequencing."
/clone_lib="Human retina cDNA randomly primed sublibrary"
/sex="mixed (males and females)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glil674
glil674
Greenchabditis elegans (strain CB1489 him-8(e1489), ) (library:
Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole animal CDNA to mRNA.
Caenorhabditis elegans
Eukaryotae; mitochondrial eukaryotaes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditidae; Caenorhabditis.
Rhabditidae; Caenorhabditis.
I (bases 1 to 317)
Kohara Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELKO94GZR 317 bp mRNA EST 1
C.elegans cDNA clone yk94g12 : 3' end, single read.
D66283
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                                                                                                                                                                                                                                                                                                                                                      56 others
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Pred. No. 6.10e-06;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole animal"
/clone_lib="ruji kohara unpublished cDNA"
82 c 64 g 85 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 tetectgettettgatetetecaetetaeatecaaceggnaageteet 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 gcaaggaaatgcagtattttatgcagcagtggactggtaccaacaa 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCACAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toward an expression map of the C.elegans genome Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="E. coli strain K802"
<1..>796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="CB1489 him-8(e1489)
/dev_stage="varied"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-Aug-1995) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Hermaphrodite, male"
                                                                                                                                                                                                                                                    /tissue_type="retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institute of Genetics
Yata 1111, Mishima Shizuoka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email:ykohara@ddbj.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 183 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.8%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 5.0%;
Local Similarity 73.9%;
nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 0559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phone: 0559-81-6854
                                                                                                                                                                                                                                                                                                                                                    181 c
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Gene Library Lab.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I oligo(dT) primer [5'
AACTGGAAGAATTGGGGGCGCCTTTTTTTTTTTTTTT 3'],
                 Contact: Wilson RK
Washu-Merck EST Project
Washu-Merck EST Project
Washu-Merck EST Project
Washu-Merck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham
High quality, sequence stop: 477.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W29026 796 bp mRNA EST 08-MAY-1996
55clO Human retina cDNA randomly primed sublibrary Homo sapiens
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Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
JS North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 137; Length 687;
Pred. No. 6.10e-06;
0; Mismatches 11; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 atacatatcagtctgcttttgtcatcttctgcagtgagcttccaacactcc 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 ATACATATCTGTG-GCTTGGGTCTTCTCCTGCATCCAGCTTGCACCACTCC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares pregnant uterus NbHPU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAGAATT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.0%;
Best Local Similarity 76.5%;
Matches 39; Conservative
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/organism="Homo sapiens"
/note="Organ: pancress; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Reference: Hum Mol Gen 2, 1795 (1993)
Takeda et al. Cloned unidirectionally. Primer: Oligo dT.
-5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
/clone="328859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T23370 360 bp mRNA EST 17-0CT-1996 508102 membrane-free polysomes from endosperm Zea mays CDNA clone 5c08h02 5' end. T23370 9511392
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Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 360)
Shen.B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,
Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
                                    Larkins, B. Partial sequencing and mapping of clones from two maize cDNA \,
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                                                                                                                                                                                                                                                                                                                                       /clone_lib="Pancreatic Islet"
/tissue_type="pancreatic islet"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 1.34e-04;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: The Maize cDNA Project
                                                                                                                                                  Location/Qualifiers
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Best Local Similarity 76.9%;
Matches 30; Conservative
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Tel: 314 286 1800
Fax: 314 286 1810
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AUTHORS
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                                                                                                                                           human clone=73829 library=Stratagene fetal spleen (#937205)
vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
primer=M13RP1 Rsitel=EcoRI Rsite2=RhoI Pooled fetal spleens. Cloned
unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb;
uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTGGCACGAGG-3'; 3'
adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTTTTT"3'.
                                                                                                                                                                                                                                                                                       Eucaryotae: Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 325)

Hillier, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read.
Location/Qualifiers
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Washerston,K., Williamson,A., Wohldmann,P. and Wilson,R. Unpublished (1995)
                    08-FEB-1995
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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0
           yb42d03.rl Homo sapiens CDNA clone 73829 5' similar to gb:J03910_rnal Human (HUMAN).
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WashU-Merck EST Project
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Location/Qualifiers
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Marra,M., Sibley,L.D., Wan,K.L. and Waterston,R.A.
Washh-Merck Toxoplasma EST Project
Unpublished (1996)
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Coxpolasma gondii

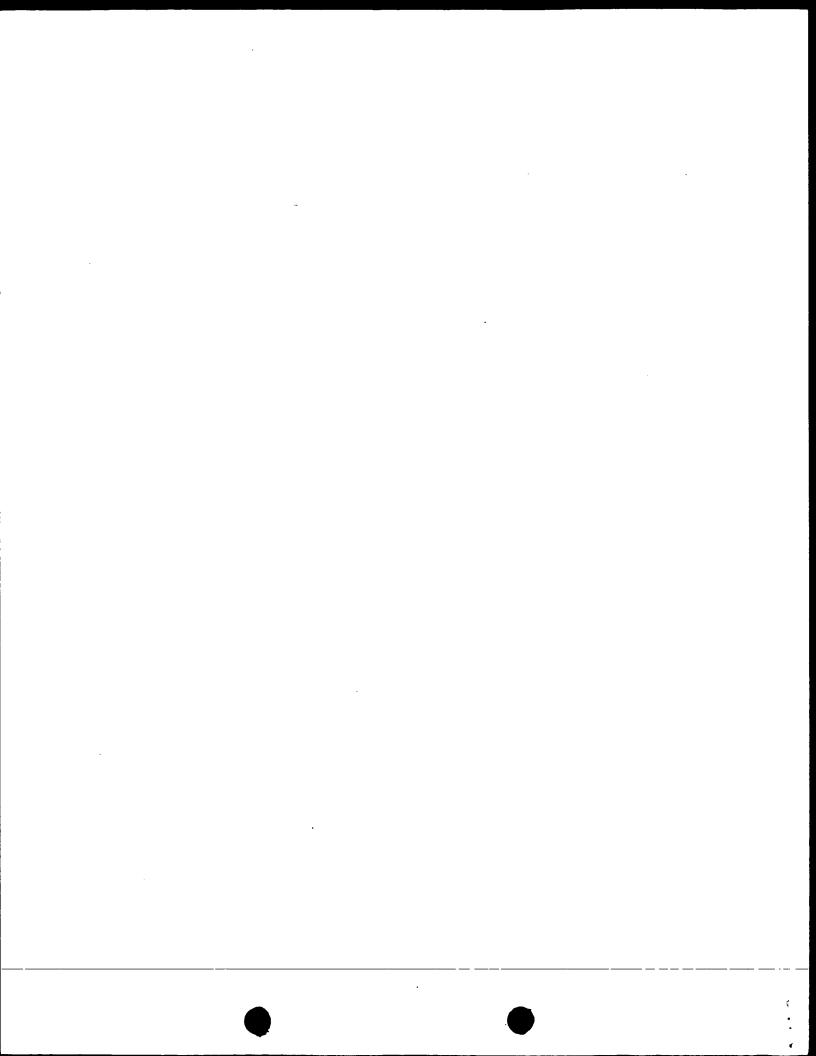
Eukaryotee; mitochondrial eukaryotes; eukaryote crown group;
Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystida;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Interdisciplinary Center for Biotechnology Research
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Pred. No. 1.34e-04;
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                                                                                                                                                                                                                                             E-mail: robferlnervm.nerdc.ufl.edu
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                                                                                                                                      Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                       University of Florida
P.O. Box 100695
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-1995
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                           LOCUS T71088 376 bp mRNA EST 01-MA
DEFINITION yc50d04.rl Homo sapiens cDNA clone 84103 5' similar to
95:J03910_rna1 Human (HUMAN);.
ACCESSION T71088
NID 9685609
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                                                                                                                         Length 371;
                                                                                                                                        Pred. No. 1.34e-04;
0; Mismatches 12; Indels
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                                                                                                                                                                                     266 gtttcgttggtgataaacatggtggagaagtccaccaacatgagc 310
                                                                                                                                                                                                                  68 GITICCIGGIGGICCACITAAIGGAGAIGICCAGAAACACGAGC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 bp mRNA EST YP23h05.s1 Homo sapiens cDNA clone 188313 3'. 9921759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
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Pred. No. 1.34e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 gtgcaaatgcactcctgcaagaagagctgctgctcct 158
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1..371
/organism="Toxoplasma gondii"
/clone="tgzy27b03.r1"
/strain="RH"
                                                                                                                           DB 99;
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                                                                                                                           Score 21;
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Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                             Source
                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                          FEATURES
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                               Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                              Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia: Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Barcopteraydi: Choanata; Tetrapoda; Amniota: Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 383)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
High quality sequence stops: 268
Source: IMAGE Consortium, LLNL; the through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human clone=188313 library-Soares breast 3NbHBst vector-pT7T3D
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1 (bases 1 to 395)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,I., Tan,F., Trevaskis,E.,
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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...34e-6; Indels
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Pred. No. 1.34e-
0; Mismatches
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                                                                                                                                                                              and M.Fatima Bonaldo.
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Local Similarity 81.8%;
nes 27; Conservative
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DEFINITION
                                                                                                                                                                                                   ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                          AUTHORS
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SOURCE
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High qulity sequence stops: 304
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                              Contact: Wilson RK
WashU-Merck EST Project
WashU-migton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                    4 others
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Pred. No. 1.34e-04;
0; Mismatches 8
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/clone="84102"
105 c 91 g 110
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                                                                                                                                                                                                                                                                                                                                                                                                             91 g
WashU-Merck EST Project
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.4%;
Matches 29; Conservative
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Human chromosome 5 LA Human chromosome 5 LA Human chromosome 5 LA 26232 Lambda-PRL2 Ara human STS SHGC-7175 c zr55911.s1 Soares NhH

HUMC5200 HUMC5200 HUMC5200 ATA67387 G14220

HS1147657

446 474 470 440 483 693 83

zr55g11.sl Soares NhH zt30e09.sl Soares ova zt30e09.sl Soares ova

HS1153832

zn69a03.sl Stratagene

Human chromosome 5 LA

5740 Arabidopsis thal

AA219045

Match Length

Score

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AT4774
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49:qneST1 50:qneST2 51:qneST3 52:qneST4 53:qneST5

54:qneST1 50:qneST2 51:qneST3 52:qneST4 53:qneST5

54:qneST1 60:qneST1 56:qneST13 62:qneST10

59:qneST1 60:qneST12 61:qneST13 62:qneST14 63:qneST10

69:qneST1 70:qneST2 71:qneST23 72:qneST24 73:qneST25

74:qneST 75:qneST2 71:qneST23 72:qneST24 73:qneST25

79:qneST5 75:qneST6 71 60:qneST1 82:qneST3 83:qneST25

79:qneST5 80:qneST6 80:qneST6 83:qneST9

84:qneST5 80:qneST6 80:qneST6 80:qneST9

84:qneST5 90:qneST6 90:qneST1 80:qneST1 80:qneST1 80:qneST1 80:qneST1 80:qneST1 80:qneST1 80:qneST1 80:qneST1 90:qneST1 90:qneST1 90:qneST1 90:qneST1 90:qneST1 90:qneST1 90:qneST1 90:qneST2 90:qneST2 90:qneST1 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST2 90:qneST
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835.145 Million cell updates/sec
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1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204

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18:EST211 14:EST217 20:EST213 16:EST219 22:EST225

23:EST221 24:EST22 25:EST223 26:EST224 27:EST225

28:EST222 29:EST223 36:EST23 36:EST239 33:EST239 33:EST231 34:EST233 36:EST233 36:EST233 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST23 36:EST33 36:EST3 36:EST33 36:EST33 36:EST3 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:EST33 36:E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by Intelligenetics, Inc.
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Listing first 45 summaries
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Gap 6
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Description:
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Comp:
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4.95e-06 1.95e-06 1.95e-04 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.93e-03 1.94e-02

human STS SHGC-32985. LD04428.5prime LD Dro

Stratagene Soares mon

Stratagene Stratagene Soares par Stratagene

mr63e09.rl mr68c01.rl

Soares mou Soares mul Soares 2Nb Soares 2Nb

mc27e09.rl yz30f08.rl

AA108214 AA138946 HS525332 AA144720 MM13311 N76192 AA200366

zp86cll.rl stratagene zn55(02.rl Stratagene m95506.rl Stratagene yv55cl2.rl Soares fet nc38fl0.rl NCI CGAP nc38fl0.rl NCI CGAP nc3810.rl NCI CGAP

HS1147808

85033344 85033334 8503334 850334 85034 85034 85034 85034 85034

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Newman T., deBruijn F.J., Green P., Keegstra K., Kende H., McIntosh L., Ohlrogge J., Raikhel N., Somerville S., Thomashow M., Retzel E., Somerville C.; Retzel E., somerville C.; Referes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA
                                                                                                                                                         Eukaryotae, mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
                                                9933235
02-FEB-1995 (Rel. 42, Created)
12-MAR-1997 (Rel. 51, Last updated, Version 15)
5740 Arabidopsis thaliana cDNA clone 113R15T7.
                    standard; RNA; EST; 472 BP.
                                                                                                                                                                                                                                                                                                                                                         clones";
Plant Physiol. 106:1241-1255(1994).
                                                                                                                                        Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                 MEDLINE; 95148729.
                                   T42477;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query

Result

3.14e-02 3.14e-02 3.14e-02

Stratagene Beddington

zq43e07.s1 mo80h01.r1

AA191607 AA208979

human STS DYS200.
mr70606.rl Stratagene
mr70606.rl Stratac-

MMAA366 AA097096

130 130 130 130 130 130 130

val0d02.rl Soares mou

Stratagene

mm46b12.rl Stratagene LD02586.5prime LD Dro LD05719.5prime LD Dro

AA209457 AA068479 AA202414 AA246779 DMAA46779 HS995331

LD Dro Beddington

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33; Conservative
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
WashU Merck EST Project
WashIndron University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through strand
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Possible reversed clone: polyT not found
Seq primer: -41ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 431)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultnan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  AGIS; | 142477; AGIS July 1995.
Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan
                                                      State University MSU-DOE-PRL, Michigan State University Plant Biology Bldg.,E. Lansing, MI Tell: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu. NCBI gi: 933235 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 gaaacagttgctgnaagctaccttgagtttgcccaagaaacccttnatnag 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GAAACGITICCICCAAAGIACCITCAITAIGACGAAGAAACCICICAICAG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 431;
                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 77; Length 472; Pred. No. 4.95e-06;
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                                                                                                                                                                                                                                                                                                      Sequence 472 BP; 126 A; 97 C; 100 G; 137 T; 12 other;
                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/clone="113K15T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21; DB 24; I Pred. No. 1.04e-04;
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                                                                                                                                                                                                                                                                               /strain="var columbia"
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Best Local Similarity 71.7%;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.68;
Marches 35; Conservative
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Homo sapiens (tissue library: LANL flow sorted chromosome 5 library in M13mp18) DNA. Homo sapiens
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/tissue_lib="LANL flow sorted chromosome 5 library in
M13mp18"
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/note="5gp"
/tissue_lib="LANL flow sorted chromosome 5 library in
Ml3mp18"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Grady D.L., Robinson D.L., Gersh M., Nickerson E., McPherson J.,
Wasmuth J.J., Overhauser J., Deaven L.L., Moyzis R.K.;
"The generation and regional localization of 303 new chromosome !
sequence-tagged sites";
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 13; Indels
                                              296 gcaaggaaatgcagtattttatgcagcagtggactgntaccaacaa 341
                                                                                      260 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCACAA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.93e-03;
                                                                                                                                                                                                                        91160700
24-JAN-1996 (Rel. 46, Created)
18-MAR-1997 (Rel. 51, Last updated, Version 3)
Human chromosome 5 LANI STS 200.
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/evidence=EXPERIMENTAL
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/evidence=EXPERIMENTAL
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Best Local Similarity 72.7%;
Matches 32; Conservative
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/organism-"Arabidopsis thaliana"
/strain-"var columbia"
/strain-evar columbia"
/note="Wector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRLZ is a CDNA library derived from equal quantitie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, hal
Wasmuth,J.J., Overhauser,J., Deaven,L.L. and Moyzis,R.K.
The generation and regional localization of 303 new chromosome sequence-tagged sites
Genomics 32 (1), 91-96 (1996)
96230329
                                                                                                                             /tissue_lib-"LANL flow sorted chromosome 5 library in M13mp18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E. Lansing,Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu Seq primer: T7.
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                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 74; Length 204; Pred. No. 1.93e-03;
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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12-MAR-1997 (Rel. 51, Last updated, Version 5)
26232 Lambda-PRL2 Arabidopsis thaliana cDNA clone 88F5T7.
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Grady, D.L., Robinson, D.L., Gersh, M., Nickerson, E., McPherson, J.,
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/tissue_lib="LANL flow sorted chromosome 5 library in
M13mp18"
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           /standard_name="LANL STS 200"
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Matches 32; Conservative
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AUTHORS
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FEATURES
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Sequence 377 Query Match

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/note="Organ: mixed (see below); Vector: pt7t3D-Pac / Pharmacial with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were mede in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-48479."
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/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Barsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; "The Washu-Merck EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest park way, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810 Email: Email: est@watson.wustl.edu This clone is available royalty-free through LiLL; contact the IMAGE Consortium (infedimage.lln.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: 41m13 fwd. ET from Amersham High quality
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27-FEB-1997 (Rel. 51, Last updated, Version 1)
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host_"DH10B
mRNA
complement(<1.>417)
Sequence 417 BP; 102 A; 90 C; 115 G; 109 T; 1 other;
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Pred. No. 1.93e-03;
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/map="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA228090;
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                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                              Matches
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
              directionally cloned with Sal-Notarms using oligo dT prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 3 by analysis on the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Camden, NJ 08103.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1995
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 degrees C for 15 seconds 62 degrees C for 23 seconds 72 degrees C for 30 seconds 30 Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
                                                                                                                                                                                                                                          Length 377;
                                                                                                                                                                                                                                                                                           0; Mismatches 11; Indels
                                                                                         /clone="88F5T7"
/clone_lib="Lambda-PRL2"
c1..>37
BP: 100 A: 93 C: 64 G: 105 T: 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIS
                                                                                                                                                                                                                                                                                                                                                     tgcacaantgcaaccacaaccgcaatcgcagccacaaccgc 217
                                                                                                                                                                                                                                                                                                                                                                                     STS sequence; primer; sequence tagged site.
                                                                                                                                                                                                                                       DB 79; L
1.93e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human STS SHGC-7175 clone pg-3149.
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                                                                                                                                                                                                                                                                 Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer A: GGGTACACTTGTCCATAGGGA
Primer B: GTCAACTCAGGCATTCCTACT
                                                                                                                                                                                                                                       Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.5 mM
50 mM
20 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catarrhini; Hominidae; Homo.
1 (bases 1 to 400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR Cycles:
Thermal Cycler:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 bp
                                                                                                                                                                                                                                          4.68;
                                                                                                                                                                                                                                                                 Local Similarity 73.2%;
nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Annealing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tris-HCl:
pH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255..348
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                                                                     CDNA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             size: 94
Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers, R.M.
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Gaps

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source

FEATURES

STS

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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Organism="Homo vary: Vector: pT713D (Pharmacia) with a modified polylinker; Site.]: Not I: Site.2: Eco RI: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT713 vector M.Fatima Bonaldo."
//clone="723880"
zt30e09.sl Soares ovary tumor NDHOT Homo sapiens cDNA clone 723880
3' slmilar to TR:G307146 G307146 PROTEIN-LYSINE OXIDASE HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: 41m13 fwd. ET from Amersham
High quality sequence stop: 174.
                                                                                                                                                                      06-MAR-1997 (Rel. 51, Created)
06-MAR-1997 (Rel. 51, Last updated, Version 1)
2t30e09.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone 723880
3' similar to TR:G307146 G307146 PROTEIN-LYSINE OXIDASE HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 66; Length 421
Pred. No. 1.93e-03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
complement(<1..>421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares ovary tumor NDHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; RNA; EST; 421 BP
                                                                                                                                                                                                                                                                                                                             Wilson, R.
The Washu-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 AAAACACTGTACAGCAAAGTG 173
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.6%;
Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
C
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                                             PRECURSOR ; .
                                                                                                                                                      Homo sapiens
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                                                                 AA235526
91859981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR ;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 12
HS1153832 ;
AA235526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91859981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
  DEFINITION
                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
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                                                                 ACCESSION
                                                                                                                                                                                                                   REFERENCE
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                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHW, pregnant uterus
NbHPU, and fetal heart NbHHJBW) were mixed and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-348479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 332.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                             Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 417)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                  AA228090 417 bp mRNA EST 24-FEB-1997 zr55911.s1 Soares NhHMPU S1 Homo sapiens cDNA clone 667364 3' similar to TR:G307146 G307146 PROTEIN-LXSINE OXIDASE HOMOLOG
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Pred. No. 1.93e-03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-Merck EST Project
      90 aaaacaacactgtagagaaaagtg 113
                           150 AAAACAACACTGTACAGCAAAGTG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .90 aaaacaacactgtagagaaaagtg 113
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Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..417
                                                                                                                                                                                                 PRECURSOR ; . AA228090 g1849624
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102
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                                                                                                                                                                                                                                                                                           human.
                                                                                                                RESULT 10
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                                                                                                                                                           DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
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Gaps

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/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/ord="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/ord="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/order of darcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni-ZAP XR
Vector. -5 adaptor sequence: 5 GAATTCGGGAGGA 3' -3'
/olone=563404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS AA191137 424 bp mRNA EST 15-JAN-1997
DEFINITION 2P86c11.rl Stratagene HeLa cell s3 937216 Homo sapiens CDNA clone 627092 5'.
ACCESSION AA191137
NID 91779831
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Location/Qualifiers
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@inage.llnl.gov) for further information. Seq primer: -40K13 fwd. from Amersham High quality sequence stop: 353.
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Eukaryotes; Metazoa; Chordata;
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 424)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
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WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/lab_host="SOLR (kanamycin resistant)"
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0; Mismatches 6;
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Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Barsons J., Riffin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;
"The washu-Merck EST Project";
                                                                                                                                                                                                         Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louls, Mo 63100 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wditson.wusl.edu This clone is available royalty-free through LINI. contact the IMAGE Consortium (info@image.llnl.gov) for turner information. Possible reversed clone: similarity on wrong strand Seg primer: -41ml3 fwd. ET from Amersham High quality
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Tel: 314 286 1800
Fax: 314 286 1810
              Verteģrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4.6%; Score 20; DB 83; Length 421
Best Local Similarity 91.7%; Pred. No. 1.93e-03;
Matches 22; Conservative 0; Mismatches 2; Indels
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/sex="Female"
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Washington University School of Medicine
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WashJ-Merck EST Project
WashJ-Merck EST Project
WashJ-Merck EST Project
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 440.
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Bukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

Bukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

Userebrata; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

Hollar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultnan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Watersfston,R., Williamson,A., Wohldmann,P. and Wilson,R.

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/lab_host="SOLR (kanamycin resistant)"
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/lab_lost="SOLR (kanamycin resistant)"
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